

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 19 Seconds  
(without alignments)  
35.448 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR\_79.\*

1: pir1.\*

2: pir2.\*

3: pir3.\*

4: pir4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	21	47.7	7	2 S33567	tubulin beta-3 cha
2	19	43.2	6	2 B35640	cerebellar degener
3	18	40.9	5	2 C53284	T-cell receptor be
4	18	40.9	7	2 E61491	seed protein ws-5
5	17	38.6	5	2 JH0253	gut pentapeptide -
6	17	38.6	7	2 S21230	dermorphin (Trp-4,
7	16	36.4	7	4 S15597	orf 4 rara 5'-regi
8	15	34.1	6	2 S66195	alcohol dehydrogen
9	14	31.8	7	2 S09652	hypothetical prote
10	13	29.5	5	2 PT0308	Ig heavy chain CRD
11	13	29.5	6	2 JN0861	peptidyl-dipeptida
12	13	29.5	6	2 A31263	dihydrofolate redu
13	13	29.5	6	2 B31263	dihydrofolate redu
14	13	29.5	7	2 PT0727	T-cell receptor be
15	13	29.5	7	2 PT0688	T-cell receptor be
16	13	29.5	7	2 S58797	serine/threonine-s
17	13	29.5	7	2 A58512	venom heptapeptide
18	13	29.5	7	4 PC2056	trichodecin I -
19	13	29.5	7	4 PC2057	trichodecin II -
20	12	27.3	3	3 A23751	spinal cord peptid
21	12	27.3	4	2 A53284	T-cell receptor be
22	12	27.3	4	2 B53284	T-cell receptor be
23	12	27.3	4	2 S47552	ubiquitin - rat
24	12	27.3	4	2 PT0706	T-cell receptor be
25	12	27.3	5	2 B61445	Leu-enkephalin - b
26	12	27.3	5	2 A61445	Met-enkephalin - b
27	12	27.3	5	2 B61168	cocoonase (EC 3.4.
28	12	27.3	5	2 PT0267	Ig heavy chain CRD
29	12	27.3	5	2 D44823	synaptosomal-assoc

30	12	27.3	5	2	PT0707	T-cell receptor be
31	12	27.3	5	2	PT0669	T-cell receptor be
32	12	27.3	5	2	PT0585	T-cell receptor be
33	12	27.3	5	2	PT0717	T-cell receptor be
34	12	27.3	5	2	C23751	spinal cord peptid
35	12	27.3	6	2	JU0355	lipopeptide WS1279
36	12	27.3	6	2	PT0280	Ig heavy chain CRD
37	12	27.3	6	2	PT0514	T-cell receptor be
38	12	27.3	6	2	PT0512	T-cell receptor be
39	12	27.3	6	2	PT0720	T-cell receptor be
40	12	27.3	6	2	PT0560	T-cell receptor be
41	12	27.3	6	2	PT0723	T-cell receptor be
42	12	27.3	6	2	PT0726	T-cell receptor be
43	12	27.3	6	2	PT0730	T-cell receptor be
44	12	27.3	6	2	A41946	T-cell receptor ga
45	12	27.3	6	2	PT0605	T-cell receptor be
46	12	27.3	7	2	A60224	Met-enkephalin-Arg
47	12	27.3	7	2	S42407	gramicidin S synth
48	12	27.3	7	2	PT0526	T-cell receptor be
49	12	27.3	7	2	PT0523	T-cell receptor be
50	12	27.3	7	2	PT0642	T-cell receptor be
51	12	27.3	7	2	PT0667	T-cell receptor be
52	12	27.3	7	2	PT0666	T-cell receptor be
53	12	27.3	7	2	PT0663	T-cell receptor be
54	12	27.3	7	2	PT0542	T-cell receptor be
55	12	27.3	7	2	PT0683	T-cell receptor be
56	12	27.3	7	2	PT0719	T-cell receptor be
57	12	27.3	7	2	PT0586	T-cell receptor be
58	12	27.3	7	2	PT0702	T-cell receptor be
59	12	27.3	7	2	PT0728	T-cell receptor be
60	12	27.3	7	2	S33244	neuromodulatory pe
61	12	27.3	7	2	S33245	neuromodulatory pe
62	12	27.3	7	2	S33246	neuromodulatory pe
63	11	25.0	3	3	E37196	bradykinin-potenti
64	11	25.0	4	2	A34626	RPCII-related neuro
65	11	25.0	4	2	PT0661	T-cell receptor be
66	11	25.0	5	2	A32516	cholecystokinin-5
67	11	25.0	5	2	A60803	neuropeptide - sea
68	11	25.0	5	2	PT0281	Ig heavy chain CRD
69	11	25.0	5	2	PT0729	T-cell receptor be
70	11	25.0	5	2	PT0703	T-cell receptor be
71	11	25.0	5	2	PT0580	T-cell receptor be
72	11	25.0	5	2	G37196	bradykinin-potenti
73	11	25.0	5	2	B34835	dnaA protein - Pse
74	11	25.0	6	2	PT0629	T-cell receptor be
75	11	25.0	6	2	PT0532	T-cell receptor be
76	11	25.0	6	2	PT0519	T-cell receptor be
77	11	25.0	6	2	PT0604	T-cell receptor be
78	11	25.0	6	2	PT0637	T-cell receptor be
79	11	25.0	6	2	PT0641	T-cell receptor be
80	11	25.0	6	2	F41946	T-cell receptor ga
81	11	25.0	6	2	PD0028	pev-kinin 2 - pena
82	11	25.0	6	2	A27696	contraction-inhibi
83	11	25.0	6	2	B27696	contraction-inhibi
84	11	25.0	6	2	A61068	locustakinin - mig
85	11	25.0	6	2	A43129	neuropeptide GNFR
86	11	25.0	6	4	I79564	hypothetical TCU3
87	11	25.0	7	2	PQ0727	H2 class I protein
88	11	25.0	7	2	E48394	glycoprotein compo
89	11	25.0	7	2	PH1602	Ig H chain V-D-J r
90	11	25.0	7	2	PT0628	T-cell receptor be
91	11	25.0	7	2	PT0543	T-cell receptor be
92	11	25.0	7	2	PT0722	T-cell receptor be
93	11	25.0	7	2	PT0689	T-cell receptor be
94	11	25.0	7	2	PX0008	glucuronosyltransf
95	11	25.0	7	2	B48394	major fat-globule
96	11	25.0	7	2	PD0029	pev-kinin 1 - pena
97	11	25.0	7	2	PN0649	pullulanase (EC 3
98	11	25.0	7	2	S57274	triacylglycerol li
99	11	25.0	7	2	A61081	tryptophyllin, bas
100	11	25.0	7	4	155382	hypothetical pepti

## ALIGNMENTS

RESULT 1  
S33567  
tubulin beta-3 chain - fruit fly (*Drosophila melanogaster*) (fragment)  
C;Species: *Drosophila melanogaster*  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 09-Jul-2004  
C;Accession: S33567  
R;Hinz, U.; Wolk, A.; Renkawitz-Pohl, R.  
Development 116, 543-554, 1992  
A;Title: Ultrabithorax is a regulator of beta-3 tubulin expression in the *Drosophila* wing  
A;Reference number: S33567; MUID:93170162; PMID:1363225  
A;Accession: S33567  
A;Status: preliminary; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-7 <HIN>  
A;Cross-references: UNIPROT:P08841; EMBL:X68393; NID:g7669; PIDN:CAA48459.1; PID:g437744  
C;Genetics:  
A;Gene: FlyBase:beta-Tub60D  
A;Cross-references: FlyBase:FBgn0003888  
A;Introns: 5/3

Query Match 47.7%; Score 21; DB 2; Length 7;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 2 GGVFW 6  
| |  
Db 3 GARFW 7

RESULT 2  
B35640  
cerebellar degeneration-related protein - mouse (fragment)  
C;Species: *Mus musculus* (house mouse)  
C;Date: 28-Sep-1990 #sequence\_revision 28-Sep-1990 #text\_change 24-Jun-1993  
C;Accession: B35640  
C;Chen, Y.T.; Rettig, W.J.; Yenamandra, A.K.; Kozak, C.A.; Chaganti, R.S.K.; Posner, J.H.  
Proc. Natl. Acad. Sci. U.S.A. 87, 3077-3081, 1990  
A;Title: Cerebellar degeneration-related antigen: a highly conserved neuroectodermal marker  
A;Reference number: A35640; MUID:90222173; PMID:2326268  
A;Accession: B35640  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-6 <CHE>

Query Match 43.2%; Score 19; DB 2; Length 6;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 5 FWQ 7  
| |  
Db 1 FWE 3

RESULT 3  
C53284  
T-cell receptor beta 2 chain D region, Dbeta2 - rabbit  
C;Species: *Oryctolagus cuniculus* (domestic rabbit)  
C;Date: 02-May-1994 #sequence\_revision 18-Nov-1994 #text\_change 05-Nov-1999  
C;Accession: C53284  
R;Harindranath, N.; Alexander, C.B.; Mage, R.G.  
Mol. Immunol. 28, 881-888, 1991  
A;Title: Evolutionarily conserved organization and sequences of germline diversity and joining regions in the T-cell receptor beta 2 chain D region  
A;Reference number: A53284; MUID:91342695; PMID:1678859  
A;Accession: C53284  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-5 <HAR>  
A;Cross-references: GB:S60737; NID:g233916; PIDN:AAB19519.1; PID:g233919  
A;Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBI:P:60740)  
C;Keywords: T-cell receptor

Query Match 40.9%; Score 18; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGG 3  
| | |  
Db 3 GGG 5

RESULT 4  
E61491  
seed protein ws-5 - winged bean (fragment)  
C;Species: *Psophocarpus tetragonolobus* (winged bean)  
C;Date: 07-Oct-1994 #sequence\_revision 07-Oct-1994 #text\_change 07-Oct-1994  
C;Accession: E61491  
R;Hirano, H.  
J. Protein Chem. 8, 115-130, 1989  
A;Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dimensional gel electrophoresis  
A;Reference number: A61491; MUID:89351606; PMID:2765119  
A;Accession: E61491  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <HIR>  
C;Keywords: glycoprotein; seed

Query Match 40.9%; Score 18; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 GGG 3  
| | |  
Db 5 GGG 7

RESULT 5  
JH0253  
gut pentapeptide - Japanese eel  
C;Species: *Anguilla japonica* (Japanese eel)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C;Accession: JH0253  
R;Vesaka, T.; Ikeda, T.; Kubota, I.; Muneoka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A;Reference number: JH0253; MUID:92062113; PMID:1953755  
A;Accession: JH0253  
A;Molecule type: protein  
A;Residues: 1-5 <UES>  
A;Experimental source: gut  
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric fundus, and of the circular muscle of the gastro-intestinal junction.

Query Match 38.6%; Score 17; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5 FW 6  
| |  
Db 2 FW 3

RESULT 6  
S21230  
dermorphin (Trp-4, Asn-7) [validated] - two-colored leaf frog (fragment)  
C;Species: *Phyllomedusa bicolor* (two-colored leaf frog)  
C;Date: 19-Mar-1997 #sequence\_revision 10-Oct-1997 #text\_change 18-Aug-2000  
C;Accession: S21230  
R;Mignogna, G.; Severini, C.; Simmaco, M.; Negri, L.; Falconieri Erspamer, G.; Kreil, G.;  
FEBS Lett. 302, 151-154, 1992  
A;Title: Identification and characterization of two dermorphins from skin extracts of the  
A;Reference number: S21152; MUID:92339502; PMID:1633846  
A;Accession: S21230  
A;Status: preliminary

A;Molecule type: protein  
A;Residues: 1-7 <MIG>

C;Superfamily: dermorphin precursor; dermorphin precursor amino-terminal homology

Query Match 38.6%; Score 17; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 FW 6

||

Db 3 FW 4

#### RESULT 7

S15597

orf 4 rara 5'-region - human

C;Species: Homo sapiens (man)

C;Date: 04-Jun-1999 #sequence\_revision 04-Jun-1999 #text\_change 28-Jun-1999

C;Accession: S15597

R;Brand, N.J.; Petkovich, M.; Chambon, P.

Nucleic Acids Res. 18, 6799-6806, 1990

A;Title: Characterization of a functional promoter for the human retinoic acid receptor-

A;Reference number: S15594; MUID:91088249; PMID:2175878

A;Accession: S15597

A;Molecule type: DNA

A;Residues: 1-7 <BRA>

A;Cross-references: EMBL:X56058; MID:g35876

A;Note: this ORF from Fig. 2 is not annotated in GenBank entry HSRARA2, release 111.0

C;Comment: This sequence is not thought to be translated.

C;Genetics:

A;Gene: GDB:RARA

A;Cross-references: GDB:120337; OMIM:180240

A;Map position: 17q12-17q12

Query Match

Best Local Similarity 36.4%; Score 16; DB 4; Length 7;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGV 4

||

Db 4 GGV 6

#### RESULT 8

S66195

alcohol dehydrogenase (EC 1.1.1.1) class III low affinity form - cod (Gadus sp.) (fragment)

C;Species: Gadus sp. (cod)

C;Date: 19-Mar-1997 #sequence\_revision 29-Aug-1997 #text\_change 12-Jun-1998

C;Accession: S66195

R;Hjelmqvist, L.; Hackett, M.; Shafiqat, J.; Danielsson, O.; Iida, J.; Hendrickson, R.C.;

FEBS Lett. 367, 237-240, 1995

A;Title: Multiplicity of N-terminal structures of medium-chain alcohol dehydrogenases. M

zyme.

A;Reference number: S66191; MUID:95331382; PMID:7607314

A;Accession: S66195

A;Molecule type: protein

A;Residues: 1-6 <HJE>

C;Superfamily: alcohol dehydrogenase; long-chain alcohol dehydrogenase homology

C;Keywords: alcohol metabolism; NAD; oxidoreductase

Query Match

Best Local Similarity 34.1%; Score 15; DB 2; Length 6;

Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFQW 7

||

Db 3 VAWW 6

#### RESULT 9

S09652

hypothetical protein (aacC2 3' region) - Enterobacter cloacae (fragment)

C;Species: Enterobacter cloacae

C;Date: 12-Feb-1993 #sequence\_revision 12-Feb-1993 #text\_change 08-Oct-1999

C;Accession: S09652

R;Vliegenthart, J.S.; Ketelaar-van Gaalen, P.A.G.; van de Klundert, J.A.M.

Antimicrob. Agents Chemother. 33, 1153-1159, 1989

A;Title: Nucleotide sequence of the aacC2 gene, a gentamicin resistance determinant invol

A;Reference number: S09651; MUID:90024972; PMID:2552900

A;Accession: S09652

A;Molecule type: DNA

A;Residues: 1-7 <VLI>

A;Cross-references: EMBL:X51534; MID:g40878; PIDN:CAA35914.1; PID:g581034

Query Match

Best Local Similarity 31.8%; Score 14; DB 2; Length 7;

Matches 1; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 VFW 6

||

Db 2 IIW 4

#### RESULT 10

PT0308

Ig heavy chain CRD3 region (clone 6-88) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 16-Aug-1996

C;Accession: PT0308

R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j

A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0308

A;Molecule type: DNA

A;Residues: 1-5 <YAM>

A;Experimental source: B lymphocyte

C;Keywords: heterotetramer; immunoglobulin

Query Match

Best Local Similarity 29.5%; Score 13; DB 2; Length 5;

Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WQ 7

||

Db 2 WE 3

#### RESULT 11

JN0861

peptidyl-dipeptidase A inhibitory peptide C111 - striped bonito

C;Species: Sarda orientalis (striped bonito)

C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999

C;Accession: JN0861

R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.

Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993

A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory pe

A;Reference number: JN0859; MUID:94080036; PMID:7764272

A;Accession: JN0861

A;Molecule type: protein

A;Residues: 1-6 <MAT>

A;Experimental source: liver

C;Comment: The carboxyl end is essential for the protein's expression of angiotensin I-co

C;Superfamily: bradykinin-potentiating peptide

C;Keywords: angiotensin-converting enzyme inhibitor

Query Match

Best Local Similarity 29.5%; Score 13; DB 2; Length 6;

Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GVF 5

||

Db 1 GVV 3

#### RESULT 12

A31263  
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum  
 C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Mar-1996  
 C;Accession: A31263  
 R;Peterson, D.S.; Walliker, D.; Wellem, T.E.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988  
 A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase  
 A;Reference number: A94217; MUID:89057886; PMID:2904149  
 A;Accession: A31263  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-6 <PET>  
 C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 29.5%; Score 13; DB 2; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WQ 7  
 |:  
 Db 3 WE 4

RESULT 13  
 B31263  
 dihydrofolate reductase (EC 1.5.1.3) / thymidylate synthase (EC 2.1.1.45) - Plasmodium falciparum  
 C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 20-Mar-1996  
 C;Accession: B31263  
 R;Peterson, D.S.; Walliker, D.; Wellem, T.E.  
 Proc. Natl. Acad. Sci. U.S.A. 85, 9114-9118, 1988  
 A;Title: Evidence that a point mutation in dihydrofolate reductase-thymidylate synthase  
 A;Reference number: A94217; MUID:89057886; PMID:2904149  
 A;Accession: B31263  
 A;Status: not compared with conceptual translation  
 A;Molecule type: DNA  
 A;Residues: 1-6 <PET>  
 C;Keywords: methyltransferase; NADP; oxidoreductase

Query Match 29.5%; Score 13; DB 2; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 WQ 7  
 |:  
 Db 3 WE 4

RESULT 14  
 PT0727  
 T-cell receptor beta chain V-D-J region (161-2F) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0727  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0727  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-6 <FEE>  
 A;Experimental source: newborn thymus, strain BALB/c  
 C;Keywords: T-cell receptor

Query Match 29.5%; Score 13; DB 2; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 GGV 4  
 |:  
 Db 3 GGL 5

RESULT 15  
 PT0688  
 T-cell receptor beta chain V-D-J region (140-1D) - mouse (fragment)  
 C;Species: Mus musculus (house mouse)  
 C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997  
 C;Accession: PT0688  
 R;Feeney, A.J.  
 J. Exp. Med. 174, 115-124, 1991  
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.  
 A;Reference number: PT0509; MUID:91277601; PMID:1711558  
 A;Accession: PT0688  
 A;Status: translation not shown  
 A;Molecule type: DNA  
 A;Residues: 1-7 <FEE>  
 A;Experimental source: day 18 fetal thymus, strain BALB/c  
 C;Keywords: T-cell receptor

Query Match 29.5%; Score 13; DB 2; Length 7;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 GGVFW 6  
 |:  
 Db 3 GDADW 7

Search completed: August 3, 2005, 11:42:31  
 Job time : 20 secs



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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 88.6667 Seconds  
(without alignments)  
40.427 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	16	36.4	7	2 Q8JE81	Q8JE81 human immun
2	14	31.8	7	2 P82445	P82445 nicotiana t
3	13	29.5	7	1 BRHP CONIM	P58803 conus imper
4	13	29.5	7	1 FAR5_HIRME	P42564 hirudo medi
5	12	27.3	5	1 PAP2_PARMA	P81864 pardachirus
6	12	27.3	5	1 UC22_MAIZE	P80628 zea mays (m
7	12	27.3	7	1 ASCL_ALLAS	P84071 allium asca
8	12	27.3	7	1 WWA1_ACHFUF	P35920 achatina fu
9	12	27.3	7	1 WWA2_ACHFUF	P35920 achatina fu
10	12	27.3	7	1 WWA3_ACHFUF	P35921 achatina fu
11	12	27.3	7	2 Q95945	Q95945 saccharonyc
12	12	27.3	7	2 O55184	O55184 rattus norv
13	12	27.3	7	2 Q63480	Q63480 rattus norv
14	11	25.0	2	1 GWA_SEPOF	P83570 sepiia offic
15	11	25.0	4	1 CCP3_OCTMI	P58649 octopus min
16	11	25.0	5	1 BRP7_BOTIN	P30425 bothrops in
17	11	25.0	5	1 RE32_LITRU	P82073 litoria rub
18	11	25.0	5	1 UF01_MOUSE	P38639 mus musculu
19	11	25.0	6	1 CIP1_MYTED	P13736 mytilus edu
20	11	25.0	6	1 CIP2_MYTED	P13737 mytilus edu
21	11	25.0	6	1 ET01_LITRU	P82096 litoria rub
22	11	25.0	6	1 FARP_MONEX	P41966 moniezia ex
23	11	25.0	6	1 LOK1_LOCM1	P41491 locusta mig
24	11	25.0	7	1 TFPY_PACDA	P83455 pachymedusa
25	11	25.0	7	1 TY51_LITRU	P82065 litoria rub
26	11	25.0	7	2 Q9BR74	Q9BR74 homo sapien
27	11	25.0	7	2 Q49223	Q49223 glycine max
28	11	25.0	7	2 Q8KMS9	Q8KMS9 enterobacte
29	11	25.0	7	2 Q8GL00	Q8GL00 borrelia bu
30	11	25.0	7	2 Q8GL04	Q8GL04 borrelia bu
31	10	22.7	6	1 SAPP_SEPOF	P83569 sepiia offic

32	10	22.7	7	1	CCF1_ENTFA	P20104 enterococcu
33	10	22.7	7	2	O99182	O99182 gnatholebia
34	9	20.5	4	1	FYR1_ANTEL	P58706 anthopleura
35	9	20.5	4	1	OCPI_OCTMI	P58648 octopus min
36	9	20.5	5	1	PSK_DAUCA	P58261 daucus caro
37	9	20.5	7	1	CIA_ENTFA	P11932 enterococcu
38	9	20.5	7	1	FAR1_HELTI	P41871 helisoma tr
39	8	18.2	4	1	FFKA_ANTEL	P58705 anthopleura
40	7	15.9	5	1	RE11_LITRU	P82070 litoria rub
41	7	15.9	5	1	RE11_LITRU	P82071 litoria rub
42	7	15.9	5	1	RE21_LITRU	P82072 litoria rub
43	7	15.9	5	1	RE31_LITRU	P82072 litoria rub
44	7	15.9	7	1	ALL2_CARMA	P81805 carcinus ma
45	7	15.9	7	1	ALL3_CARMA	P81806 carcinus ma
46	7	15.9	7	1	ALL4_CARMA	P81807 carcinus ma
47	7	15.9	7	1	ALL5_CARMA	P81808 carcinus ma
48	7	15.9	7	1	ALL7_CVDPO	P82158 cydia pomon
49	7	15.9	7	1	LANC_CARUI	P36960 carnobacter
50	7	15.9	7	1	PPH2_LYCES	P83379 lycopersico
51	7	15.9	7	1	UN06_PINPS	P81675 pinus pinas
52	7	15.9	7	2	Q9C5B3	Q9C5B3 arabidopsis
53	7	15.9	7	2	O50556	O50556 actinobacil
54	7	15.9	7	2	Q07624	Q07624 rous sarcom
55	6	13.6	3	1	GRWM_HUMAN	P01157 homo sapien
56	6	13.6	4	1	ACH1_ACHFUF	P35904 achatina fu
57	6	13.6	4	1	DCML_PSECH	P19916 pseudomonas
58	6	13.6	4	1	BOS1_HUMAN	P02731 homo sapien
59	6	13.6	4	1	FAR3_HIRME	P42562 hirudo medi
60	6	13.6	4	1	FAR4_HIRME	P42563 hirudo medi
61	6	13.6	4	1	FLRF_HIRME	P42561 hirudo medi
62	6	13.6	4	1	FLRN_ANTEL	P58707 anthopleura
63	6	13.6	4	1	FMRF_MACNI	P01162 macrocallis
64	6	13.6	4	2	Q16047	Q16047 homo sapien
65	6	13.6	5	1	AP21_EISFO	P84182 eisenia foe
66	6	13.6	5	1	EI03_LITRU	P82099 litoria rub
67	6	13.6	5	1	EI04_LITRU	P82100 litoria rub
68	6	13.6	5	1	FARP_ARTTR	P41853 artiposthi
69	6	13.6	5	1	FARP_CHICK	P83308 gallus gall
70	6	13.6	5	1	SUGA_ACHDO	P19991 achemeta dome
71	6	13.6	5	1	TPIS_CANFA	P54714 canis famil
72	6	13.6	5	1	UXA4_CHLTR	P38005 chlamydia t
73	6	13.6	6	1	PYF1_PENMO	P84005 penaeus mon
74	6	13.6	7	1	EI05_LITRU	P82101 litoria rub
75	6	13.6	7	1	FAF1_ASCSU	P31889 ascaris suu
76	6	13.6	7	1	FAF2_ASCSU	P67879 ascaris suu
77	6	13.6	7	1	FAF2_PANRE	P67880 panagrellus
78	6	13.6	7	1	FAR1_MACRS	P83274 macrobrachi
79	6	13.6	7	1	FAR1_PROCL	P38499 procambarus
80	6	13.6	7	1	FAR2_PROCL	P38498 procambarus
81	6	13.6	7	1	FAR3_HAECC	P81298 haemochus
82	6	13.6	7	1	FAR3_PANRE	P41874 panagrellus
83	6	13.6	7	1	FAR4_PANRE	P41875 panagrellus
84	6	13.6	7	1	FARB_CALVO	P41866 calliphora
85	6	13.6	7	1	HY7_PIG	P01153 sus scrofa
86	6	13.6	7	1	IGAO_DACDE	P06294 dactylinum d
87	6	13.6	7	1	MNPI_LEPDE	P42994 leptinotars
88	6	13.6	7	1	UF04_MOUSE	P38642 mus musculu
89	6	13.6	7	1	UH11_RAT	P56576 rattus norv
90	6	13.6	7	2	Q15903	Q15903 homo sapien
91	6	13.6	7	2	O98866	O98866 spinacia ol
92	6	13.6	7	2	Q8MPY6	Q8MPY6 taraxacum (
93	6	13.6	7	2	O07354	O07354 synechococc
94	6	13.6	7	2	O34028	O34028 sphingomona
95	6	13.6	7	2	Q8KMS3	Q8KMS3 klebsiella
96	6	13.6	7	2	Q47029	Q47029 enterobacte
97	6	13.6	7	2	Q47505	Q47505 escherichia
98	6	13.6	7	2	Q8K3H6	Q8K3H6 rattus norv
99	6	13.6	7	2	Q9YQ10	Q9YQ10 transmissib
100	5	11.4	3	1	THYL_BOMOR	P62970 bombina ori

ALIGNMENTS

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RESULT 1
Q8UEB1
ID Q8UEB1 PRELIMINARY; PRT; 7 AA.
AC Q8UEB1
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DE Bromoheptapeptide Im.
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DE Truncated pol protein (Fragment).
GS Name-pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retroviral viruses; Retroviridae; Lentivirus.
NCBI_TaxID=11676;
[1]
SEQUENCE FROM N.A.
MEDLINE=22056123; PubMed=12060770; DOI=10.1073/pnas.112177799;
RA Beerewinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RA Hoffmann D., Korn K., Selbig J.;
RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347267; AA32344.1; -.
FT NON TER 1
SQ SEQUENCE 7 AA; 885 MW; 76C37731A046C700 CRC64;

Query Match 36.4%; Score 16; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 WQ 7
Db 6 WQ 7

RESULT 2
P82445
ID P82445 PRELIMINARY; PRT; 7 AA.
AC P82445
DT 01-JUN-2000 (TrEMBLrel. 14, Created)
DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 10 kDa cell wall protein (Fragment).
OS Nicotiana tabacum (Common tobacco).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC lamiales; Solanales; Solanaceae; Nicotiana.
NCBI_TaxID=4097;
[1]
SEQUENCE.
RC STRAIN=cv. PETIT HAVANA;
RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
RA Wojtaszek P., Bolwell G.P.;
RT "Proteomic study of secondary cell wall proteins from transformed
RT tobacco culture.";
RL Planta 0:0-0(2000).
CC -1- SUBCELLULAR LOCATION: CELL WALL.
CC -1- TISSUE SPECIFICITY: XYLEM.
DR GO; GO:0005618; C:cell wall; IEA.
KW Cell wall.
FT NON TER 7
SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;

Query Match 31.8%; Score 14; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVF 5
Db 4 GHVF 7

RESULT 3
BRHP_CONIM
ID BRHP_CONIM STANDARD; PRT; 7 AA.
AC P58803;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Bromoheptapeptide Im.
OS Conus imperialis (Imperial cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypsogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
NCBI_TaxID=35631;
[1]
SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
RP TISSUE=Venom;
RX MEDLINE=97184108; PubMed=9030520; DOI=10.1074/jbc.272.8.4689;
RA Craig A.G., Jimenez E.C., Dykert J., Nielsen D.B., Gulyas J.,
RA Abogadie F.C., Porter J., Rivier J.E., Cruz L.J., Olivera B.M.,
RA McIntosh J.M.;
RT "A novel post-translational modification involving bromination of
RT tryptophan. Identification of the residue, L-6-bromotryptophan, in
RT peptides from Conus imperialis and Conus radiatus venom.";
RL J. Biol. Chem. 272:4689-4698(1997).
CC -1- FUNCTION: Does not elicit gross behavioral symptoms when injected
CC centrally or peripherally in mice.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=853.19; METHOD=LSI; RANGE=1-7; NOTE=Ref.1.
DR PIR; A58512; A58512.
KW Amidation; Bromination; Direct protein sequencing;
FT DISULFID 2 7
FT MOD RES 1 1 Pyrrolidone carboxylic acid.
FT MOD RES 6 6 6'-bromotryptophan.
FT MOD RES 7 7 Cysteine amide.
SQ SEQUENCE 7 AA; 795 MW; 6EA37DC6D87EA6B0 CRC64;

Query Match 29.5%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 GVFW 6
Db 3 GQAW 6

RESULT 4
FAR5_HIRME
ID FAR5_HIRME STANDARD; PRT; 7 AA.
AC P42564;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRamide-like neuropeptide GGYMRF-amide.
OS Hirudo medicinalis (Medicinal leech).
OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinida; Hirudinea;
OC Arhynchobdellida; Hirudiniformes; Hirudinidae; Hirudo.
NCBI_TaxID=6421;
[1]
SEQUENCE.
RP MEDLINE=92195954; PubMed=1686933; DOI=10.1016/0196-9781(91)90035-N;
RA Evans B.D., Pohl J., Kartsonis M.A., Calabrese R.L.;
RT "Identification of Rfamide neuropeptides in the medicinal leech.";
RL Peptides 12:897-908(1991).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide)
CC family.
KW Amidation; Direct protein sequencing; Neuropeptide.
FT MOD RES 7 7 Phenylalanine amide.
SQ SEQUENCE 7 AA; 858 MW; 69D4068B53387810 CRC64;

Query Match 29.5%; Score 13; DB 1; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

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Qy 2 GGVF 5  
| :  
Db 1 GGVK 4

RESULT 5  
PAP2\_PAPMA  
ID\_PAP2\_PAPMA STANDARD; PRT; 5 AA.  
AC P81864;  
DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Pardaxin II (PXII) (Fragment).  
OS Pardaxin marmoratus (Red sea moses sole).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;  
OC Soleoidae; Soleidae; Pardachirus.  
OX NCBI\_TaxID=31087;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RX MEDLINE=87057369; PubMed=3782138;  
RA Lazarovici P., Primor N., Loew L.M.;  
RT "Purification and pore-forming activity of two hydrophobic  
RT polypeptides from the secretion of the Red sea moses sole (Pardachirus  
RT marmoratus).";  
RL J. Biol. Chem. 261:16704-16713 (1986).  
CC -!- FUNCTION: Exhibits unusual shark repellent and surfactant  
CC properties. Forms voltage-dependent, ion-permeable channels in  
CC membranes. At high concentration causes cell membrane lysis.  
CC -!- SUBUNIT: Monomer. In aqueous solution exists as a tetramer.  
CC -!- SUBCELLULAR LOCATION: Secreted.  
CC -!- SIMILARITY: Belongs to the pardaxin family.  
KW Direct protein sequencing; Toxin.  
FT NON TER 5  
SQ SEQUENCE 5 AA; 614 MW; 7769C9C8100000 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 5;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 GGVF 6  
| :  
Db 1 GFFF 4

RESULT 6  
UC22\_MAIZE  
ID\_UC22\_MAIZE STANDARD; PRT; 5 AA.  
AC P80628;  
DT 01-OCT-1996 (Rel. 34, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 474)  
DE (Fragment).  
OS Zea mays (Maize).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;  
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.  
OX NCBI\_TaxID=4577;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Coleoptile;  
RA Touzet P., Riccardi F., Morin C., Damerval C., Huet J.-C.,  
RA Pernollet J.-C., Zivy M., de Vienne D.;  
RT "The maize two dimensional gel protein database: towards an integrated  
RT genome analysis program."  
RL Theor. Appl. Genet. 93:997-1005 (1996).  
CC -!- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 6.1, its MW is: 30.4 kDa.  
DR Maize-2DPAGE; P80628; COLEOPTILE.

DR MaizeDB; 123954; -.  
KW Direct protein sequencing.  
FT NON TER 1  
FT NON TER 5  
SQ SEQUENCE 5 AA; 654 MW; 72CB19C9C0300000 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 5;  
Best Local Similarity 25.0%; Pred. No. 1.6e+06;  
Matches 1; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VFWQ 7  
| :  
Db 1 IFPE 4

RESULT 7  
ASCL\_ALLAS  
ID\_ASCL\_ALLAS STANDARD; PRT; 7 AA.  
AC P84071;  
DT 25-OCT-2004 (Rel. 45, Created)  
DT 25-OCT-2004 (Rel. 45, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Ascalin (Fragment).  
OS Allium ascalonicum (Shallot) (Allium cepa var. aggregatum).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; Liliopsida; Asparagales; Alliaceae;  
OC Allium.  
OX NCBI\_TaxID=28911;  
RN [1]  
RP SEQUENCE, AND FUNCTION.  
RC TISSUE=Bulb;  
RX PubMed=12126728; DOI=10.1016/S0196-9781(02)00032-3;  
RA Wang H.X., Ng T.B.;  
RT "Ascalin, a new anti-fungal peptide with human immunodeficiency virus  
RT type 1 reverse transcriptase-inhibiting activity from shallot bulbs."  
RL Peptides 23:1025-1029 (2002).  
CC -!- FUNCTION: Has antifungal activity against B.cinerea. Inhibits HIV-  
CC 1 reverse transcriptase.  
CC -!- MISCELLANEOUS: Inhibits HIV-1 reverse transcriptase with an IC(50)  
CC of 10 uM.  
KW Direct protein sequencing; Fungicide.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 712 MW; 687866D87EA6CB30 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GG 2  
| :  
Db 6 GG 7

RESULT 8  
WWAI\_ACHFU  
ID\_WWAI\_ACHFU STANDARD; PRT; 7 AA.  
AC P35919;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE WWamide-1.  
OS Achatina fulica (Giant African snail).  
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
OX NCBI\_TaxID=6530;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Ganglion;  
RX MEDLINE=93265912; PubMed=8495720; DOI=10.1016/0014-5793(93)81458-C;  
RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
RT "WWamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
RT ganglia of the African giant snail, Achatina fulica."  
RL FEBS Lett. 323:104-108 (1993).

CC -i- FUNCTION: Exhibits modulatory effects on the peripheral nervous system. Inhibits activity on a central neuron.  
 DR PIR; S33245; S33245.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 7 Tryptophan amide.  
 SQ SEQUENCE 7 AA; 993 MW; 7362D5B69B041310 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Indels 0; Gaps 0;

Qy 6 WQ 7  
 |:  
 Db 1 WR 2

RESULT 9  
 WWA2 ACHFU STANDARD; PRT; 7 AA.  
 ID WWA2 ACHFU STANDARD; PRT; 7 AA.  
 AC P35920; 1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Wamide-2.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720; DOI=10.1016/0014-5793(93)81458-C;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 ganglia of the African giant snail, Achatina fulica.";  
 RL FEBS Lett. 323:104-108(1993).  
 DR PIR; S33246; S33246.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 7 Tryptophan amide.  
 SQ SEQUENCE 7 AA; 964 MW; 7362D5B686D32310 CRC64;

Query Match 27.3%; Score 12; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WQ 7  
 |:  
 Db 1 WK 2

RESULT 10  
 WWA3 ACHFU STANDARD; PRT; 7 AA.  
 ID WWA3 ACHFU STANDARD; PRT; 7 AA.  
 AC P35921; 1994 (Rel. 29, Created)  
 DT 01-JUN-1994 (Rel. 29, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Wamide-3.  
 OS Achatina fulica (Giant African snail).  
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Stylommatophora;  
 OC Sigmurethra; Achatinoidea; Achatinidae; Achatina.  
 OX NCBI\_TaxID=6530;  
 RN [1]  
 RP SEQUENCE.  
 RC TISSUE=Ganglion;  
 RX MEDLINE=93265912; PubMed=8495720; DOI=10.1016/0014-5793(93)81458-C;  
 RA Minakata H., Ikeda T., Muneoka Y., Kobayashi M., Nomoto K.;  
 RT "Wamide-1, -2 and -3: novel neuromodulatory peptides isolated from  
 ganglia of the African giant snail, Achatina fulica.";  
 RL FEBS Lett. 323:104-108(1993).  
 DR PIR; S33244; S33244.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 7 Tryptophan amide.

SQ SEQUENCE 7 AA; 965 MW; 7362D5B69B132310 CRC64;  
 Query Match 27.3%; Score 12; DB 1; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WQ 7  
 |:  
 Db 1 WK 2

RESULT 11  
 Q9S945 PRELIMINARY; PRT; 7 AA.  
 ID Q9S945 PRELIMINARY; PRT; 7 AA.  
 AC Q9S945; 1997 (T-EMBLrel. 02, Created)  
 DT 01-FEB-1997 (T-EMBLrel. 02, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE Inside intron 5 (Fragment).  
 OS Saccharomyces cerevisiae (Baker's yeast).  
 OC Mitochondrion.  
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
 OX NCBI\_TaxID=4932;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=D273-10B;  
 RX MEDLINE=81069885; PubMed=6254986;  
 RA Bonitz S.G., Coruzzi G., Thalenfeld B., Tzagoloff A., Macino G.;  
 RT "Assembly of the mitochondrial membrane system: Structure and  
 nucleotide sequence of the gene coding for subunit 1 of yeast  
 cytochrome oxidase.";  
 RL J. Biol. Chem. 255:11927-11941(1980).  
 DR EMBL; V00694; CAA24066.1; -;  
 DR GO; GO:0005739; C:mitochondrion; IEA.  
 KW Mitochondrion.  
 FT NON\_TER 1  
 SQ SEQUENCE 7 AA; 859 MW; 75B7232362CDC460 CRC64;

Query Match 27.3%; Score 12; DB 2; Length 7;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 WQ 7  
 |:  
 Db 4 WK 5

RESULT 12  
 O55184 PRELIMINARY; PRT; 7 AA.  
 ID O55184 PRELIMINARY; PRT; 7 AA.  
 AC O55184; 1998 (T-EMBLrel. 06, Created)  
 DT 01-JUN-1998 (T-EMBLrel. 06, Last sequence update)  
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)  
 DE Orphan receptor TR4-NS (Fragment).  
 GN Names=TR4;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=96198747; PubMed=8612486; DOI=10.1210/en.137.5.1562;  
 RA Yoshikawa T., Makino S., Gao X.M., Xing G.Q., Chuang D.M.,  
 RA Detera-Wadleigh S.D.;  
 RT "Splice variants of rat TR4 orphan receptor: differential expression  
 of novel sequences in the 5'-untranslated region and C-terminal  
 domain.";  
 RL Endocrinology 137:1562-1571(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.

RC STRAIN=Sprague-Dawley;  
 RX MEDLINE=96299786; PubMed=8661150; DOI=10.1006/geno.1996.0368;  
 RA Yoshikawa T., DuPont B.R., Leach R.J., Detera-Wadleigh S.D.;  
 RT "Isolation and identification of a novel Ala-Pro-Gly-Trip-amide-related  
 peptide inhibiting the motility of the mature oviduct in the  
 RT expression and chromosomal localization of the human gene."; TR4:  
 RL Genomics 35:361-366(1996).  
 DR EMBL; U59454; AAB91433.1; --  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER  
 SQ SEQUENCE 1 1 1 663 MW; 6DDAA878EB05350 CRC64;  
 Query Match 27.3%; Score 12; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GG 2  
 Db ||  
 4 GG 5

RESULT 13  
 Q63480 PRELIMINARY; PRT; 7 AA.  
 ID Q63480  
 AC Q63480  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE TR4-NS orphan receptor (Fragment).  
 GN Name=TR4;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96198747; PubMed=8612486; DOI=10.1210/en.137.5.1562;  
 RA Yoshikawa T., Makino S., Gao X.M., King G.Q., Chuang D.M.,  
 RA Detera-Wadleigh S.D.;  
 RT "Splice variants of rat TR4 orphan receptor: differential expression  
 RT of novel sequences in the 5'-untranslated region and C-terminal  
 RT domain";  
 RL Endocrinology 137:1562-1571(1996).  
 DR EMBL; U59125; AAB02827.1; --  
 DR GO; GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON\_TER  
 SQ SEQUENCE 1 1 1 758 MW; 672AA87864005350 CRC64;  
 Query Match 27.3%; Score 12; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 GG 2  
 Db ||  
 4 GG 5

RESULT 14  
 GWA SEPOF  
 ID GWA SEPOF STANDARD; PRT; 2 AA.  
 AC P83570;  
 DT 29-MAR-2004 (Rel. 43, Created)  
 DT 29-MAR-2004 (Rel. 43, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Neuropeptide GWA.  
 OS Sepia officinalis (Common cuttlefish).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Decapodiformes; Sepioidae; Sepiidae; Sepia.  
 OX NCBI\_TaxID=6610;  
 RN [1]  
 RP SEQUENCE, FUNCTION, MASS SPECTROMETRY, AND AMIDATION.  
 RC TISSUE=Optic lobe;

RX MEDLINE=98100358; PubMed=9437704; DOI=10.1016/S0196-9781(97)00241-6;  
 RA Henry J., Favrel P., Boucaud-Camou E.;  
 RT "Isolation and identification of a novel Ala-Pro-Gly-Trip-amide-related  
 peptide inhibiting the motility of the mature oviduct in the  
 RT cuttlefish, Sepia officinalis."; TR4:  
 RL Peptides 18:1469-1474(1997).  
 CC -1- FUNCTION: Regulatory neuropeptide with myotropic activity  
 CC targeting the distal oviduct. Inhibits the motility of the oviduct  
 CC by decreasing tonus, frequency and amplitude of contractions.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- MASS SPECTROMETRY: MW=259.9; METHOD=MALDI; RANGE=1-2; NOTE=Ref.1.  
 KW Amidation; Direct protein sequencing; Neuropeptide.  
 FT MOD\_RES 2 2 2 Tryptophan amide.  
 SQ SEQUENCE 2 AA; 261 MW; 7378100000000000 CRC64;  
 Query Match 25.0%; Score 11; DB 1; Length 2;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 W 6  
 Db 2 W 2

RESULT 15  
 OCP3 OCTMI STANDARD; PRT; 4 AA.  
 ID OCP3 OCTMI  
 AC P58649;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Cardioactive peptides Ocp-3/Ocp-4.  
 OS Octopus minor (Octopus).  
 OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;  
 OC Octopodiformes; Octopoda; Incirrata; Octopodidae; Octopus.  
 OX NCBI\_TaxID=89766;  
 RN [1]  
 RP SEQUENCE, SYNTHESIS, MASS SPECTROMETRY, AND CHARACTERIZATION.  
 RC TISSUE=Brain;  
 RX MEDLINE=20336815; PubMed=10876044; DOI=10.1016/S0196-9781(00)00201-1;  
 RA Iwakoshi E., Hisada M., Minakata H.;  
 RT "Cardioactive peptides isolated from the brain of a Japanese octopus,  
 RT Octopus minor.";  
 RL Peptides 21:623-630(2000).  
 CC -1- FUNCTION: Cardioactive; has both positive chronotropic and  
 CC inotropic effects on the heart. Ocp-4 is a 1000 time less active  
 CC than Ocp-3.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- PTM: Ocp-4 has D-Ser instead of L-Ser.  
 CC -1- MASS SPECTROMETRY: MW=395.2; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.  
 KW D-amino acid; Direct protein sequencing; Hormone.  
 FT MOD\_RES 2 2 2 D-serine (in form Ocp-4).  
 SQ SEQUENCE 4 AA; 463 MW; 6AB365B810000000 CRC64;

Query Match 25.0%; Score 11; DB 1; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 6 W 6  
 Db 3 W 3

Search completed: August 3, 2005, 12:07:37  
 Job time : 92.6667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 96.3333 Seconds  
(without alignments)  
28.104 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 121728

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_16Dec04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	7	4	AAB30895 Peptide w
2	44	100.0	7	4	AAB50797 Heart hom
3	32	72.7	7	5	ABG77517 Targettin
4	30	68.2	7	2	AAB69090 Neuronal
5	27	61.4	7	2	AAW10773 Ferritin
6	27	61.4	7	2	AAW48924 Membrane
7	26	59.1	7	7	ADL17233 Phage-dis
8	25	56.8	5	2	AAW58581 Kojibiose
9	25	56.8	7	2	AAW39859 Heavy cha
10	25	56.8	7	2	AAW39874 Heavy cha
11	25	56.8	7	2	AAW39862 Heavy cha
12	25	56.8	7	2	AAW40897 Leader se
13	25	56.8	7	2	AAW40897 Heavy cha
14	25	56.8	7	5	AAU81231 Human trk
15	24	54.5	5	5	AAU86976 Estradiol
16	24	54.5	6	3	AAW24307 Prostata
17	24	54.5	6	7	ADB78553 Rat F997-
18	24	54.5	6	8	ADN88732 Human can
19	24	54.5	6	8	ADQ68126 Cancer re
20	24	54.5	7	2	AAW10805 Ferritin
21	24	54.5	7	4	AGG62835 Amino aci
22	24	54.5	7	5	AAE24737 Yeast Vbe
23	24	54.5	7	5	ABG77610 Targettin
24	23	52.3	6	2	AAW20447 Anti-b-en
25	23	52.3	6	5	AAW49437 Penicilli

26	23	52.3	7	7	ADE78402 Peptide (
27	23	52.3	6	8	ABM79662 Peptide c
28	23	52.3	7	4	AGG62839 Amino aci
29	23	52.3	7	5	AAE24741 Yeast Vbe
30	23	52.3	7	6	AAO23874 Protein t
31	23	52.3	7	7	ADL17111 Phage-dis
32	23	52.3	7	8	ABM79691 HIV Vpr m
33	22	50.0	5	2	AAW41532 Pseudomon
34	22	50.0	5	5	ABJ11441 Human 125
35	22	50.0	5	6	ABU72672 Novel pro
36	22	50.0	5	6	ABJ39336 Human leu
37	22	50.0	5	6	ABJ56989 184P182 r
38	22	50.0	5	7	ADK41621 Synthetic
39	22	50.0	5	7	ADK41622 Synthetic
40	22	50.0	5	8	ADL12005 D-peptide
41	22	50.0	5	8	ADO63921 Human 213
42	22	50.0	5	8	AAW93214 Zona Pell
43	22	50.0	6	2	AAW03265 Viral int
44	22	50.0	6	2	AAW87430 Peptide d
45	22	50.0	6	2	AAW87395 Peptide d
46	22	50.0	6	2	AAW87396 Peptide d
47	22	50.0	6	2	AAW18678 Peptide S
48	22	50.0	6	4	AAW62355 S. saliva
49	22	50.0	6	7	ADJ76842 CDR seque
50	22	50.0	6	7	ADK41616 Synthetic
51	22	50.0	6	7	ADK41678 VP072 fib
52	22	50.0	7	1	AAW10088 Sequence
53	22	50.0	7	1	AAW61021 Peptide 1
54	22	50.0	7	2	AAW40895 Leader se
55	22	50.0	7	2	AAW87420 Peptide d
56	22	50.0	7	2	AAW49004 Membrane
57	22	50.0	7	5	ABG77601 Targettin
58	22	50.0	7	7	ADW79644 Parapoxvi
59	22	50.0	7	7	ADE15528 Melanoma
60	22	50.0	7	7	ADK41615 Synthetic
61	22	50.0	7	8	ADP13142 Prion pro
62	22	50.0	7	8	ADP75070 Parapoxvi
63	21	47.7	4	2	AAW71194 Peptide u
64	21	47.7	4	5	ABG77506 Targettin
65	21	47.7	5	2	AAW56251 Inulinase
66	21	47.7	5	4	AAW60684 Pyrococcu
67	21	47.7	5	5	AAW85447 Human col
68	21	47.7	6	2	AAW20451 Anti-b-en
69	21	47.7	6	2	AAW87436 Peptide d
70	21	47.7	6	2	AAW55114 ATCC HB 1
71	21	47.7	6	3	AAW86860 Human hae
72	21	47.7	6	3	AAW86359 Human gen
73	21	47.7	6	4	AAW82651 All-D pep
74	21	47.7	6	5	AAW79534 TCR beta-
75	21	47.7	6	5	AAW79531 TCR beta-
76	21	47.7	6	6	AAW35470 Abeta pep
77	21	47.7	6	6	ABO53504 Novel hum
78	21	47.7	6	8	ADQ37294 Vaccine a
79	21	47.7	7	2	AAW87374 Peptide d
80	21	47.7	7	3	AAW13312 Caenorhab
81	21	47.7	7	4	AAU08364 Antibody
82	21	47.7	7	5	ABG77635 Targettin
83	21	47.7	7	5	ABG77603 Targettin
84	21	47.7	7	5	ABG77643 Targettin
85	21	47.7	7	5	ABG77644 Targettin
86	21	47.7	7	5	ABG77642 Targettin
87	21	47.7	7	5	ABG77641 Targettin
88	21	47.7	7	6	ABJ39365 Human leu
89	21	47.7	7	7	ABO33846 Anti-GPI-
90	21	47.7	7	8	ADP90499 Exemplary
91	21	47.7	7	8	ADL95882 Human pro
92	20	45.5	5	4	AAW70984 Melanoco
93	20	45.5	5	5	AAO15574 Vaccine a
94	20	45.5	5	8	ADG45011 Pentapept
95	20	45.5	6	2	ADH68248 Human G-p
96	20	45.5	6	2	AAW62537 Fibronect
97	20	45.5	6	2	AAW55073 Fibronect
98	20	45.5	6	2	AAW55072 Fibronect

99 20 45.5 6 2 AAR69252 Aar69252 Endotheli  
100 20 45.5 6 2 AAW40885 Aaw40885 Leader se

## ALIGNMENTS

RESULT 1  
AAB30895  
ID AAB30895 standard; peptide; 7 AA.  
XX  
AC AAB30895;  
XX  
DT 02-APR-2001 (first entry)  
XX  
DE Peptide which selectively binds to normal cardiac endothelium.  
XX  
KW Cardiac endothelium; angiogenic factor; vascular endothelium;  
KW peripheral vascular disease; cardiovascular disease; angiogenesis;  
KW cardiac neovascularisation.

XX Unidentified.  
XX WO200075329-A1.  
XX 14-DEC-2000.  
XX 31-MAY-2000; 2000WO-US014988.  
XX 07-JUN-1999; 99US-00327045.  
XX (EDWA-) EDWARDS LIFESCIENCES CORP.  
PA (BAXT) BAXTER AG.  
XX  
PI Levine AJ, Mitterer A, Falkner F, Scheiflinger F, Dorner F;  
XX WPI; 2001-091212/10.  
XX

XX New chimeric molecules having an angiogenic factor linked to a targeting  
PT molecule that binds to a vascular endothelium, useful for increasing  
PT cardiac neovascularization, or treating peripheral vascular and  
PT cardiovascular diseases.

PS Disclosure; Page 27; 67pp; English.

XX  
CC AAB30895-99 represent targeting molecules, which are used to produce the  
CC chimeric molecules of the invention. AAB30895-98 selectively bind to  
CC normal cardiac endothelium. The specification describes a chimeric  
CC molecule comprising an angiogenic factor linked to a targeting molecule  
CC that specifically binds to a vascular endothelium. The chimeric molecules  
CC are useful for treatment of peripheral vascular or cardiovascular  
CC diseases. Specifically, they are useful for inducing or inhibiting  
CC angiogenesis, for increasing cardiac neovascularisation in ischemic  
CC tissue in the peripheral vascular system

XX Sequence 7 AA;

Query Match 100.0%; Score 44; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7  
|||  
Db 1 GGGVFWQ 7

RESULT 2  
AAB50797  
ID AAB50797 standard; peptide; 7 AA.  
XX  
AC AAB50797;  
XX  
DT 21-MAR-2001 (first entry)

XX Heart homing peptide SEQ ID NO: 2.  
DE  
XX  
KW Heart homing peptide; cardiovascular disease; ischaemic disease;  
KW gene therapy.  
XX  
OS Synthetic.

XX WO200075174-A1.  
XX 14-DEC-2000.  
XX 31-MAY-2000; 2000WO-US015088.  
XX 07-JUN-1999; 99US-00326718.

XX (BURN-) BURNHAM INST.

XX Ruoslahti E, Mackenna DA;

XX WPI; 2001-071059/08.

XX Novel heart homing peptide that selectively homes to normal ischemic and  
XX cardiac tissue useful for targeting ischemic tissues for treating  
XX ischemic and cardiovascular diseases such as atherosclerosis and  
XX restenosis.

XX Claim 2; Page 55; 70pp; English.

XX The present invention provides a number of heart homing peptides which  
XX selectively home to cardiac tissue. These can be used in the treatment of  
XX cardiovascular and ischemic diseases, such as atherosclerosis, myocardial  
XX thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial  
XX hypertrophy, congenital heart diseases, ischemic heart disease and  
XX anginas, acquired valvular/endocardial diseases, primary myocardial  
XX diseases, cardiac tumours and arrhythmias

XX Sequence 7 AA;

Query Match 100.0%; Score 44; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7  
|||  
Db 1 GGGVFWQ 7

RESULT 3  
ABG77517  
ID ABG77517 standard; peptide; 7 AA.

XX ABG77517;

XX 05-NOV-2002 (first entry)

XX Targetting peptide selective for human organ, tissue or cell type #50.

XX Human; cytostatic; antiinflammatory; antidiabetic; cardiovascular;  
XX immunomodulator; antibacterial; antiviral; gene therapy; cancer;  
KW arthritis; diabetes; inflammatory disease; atherosclerosis;  
KW autoimmune disease; bacterial infection; viral infection;  
KW cardiovascular disease; degenerative disease.

XX Homo sapiens.

XX WO200202723-A2.

XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028044.

XX 08-SEP-2000; 2000US-0231266P.



PR 17-JAN-2001; 2001US-00765101.  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 PI Arap W, Pasqualini R;  
 XX WPI; 2002-599247/64.  
 XX New targeting peptides identified by phage display, useful for treating a  
 PT disease state, e.g. cancer, diabetes, inflammatory disease,  
 PT atherosclerosis, autoimmune disease, bacterial or viral infection or  
 PT cardiovascular disease.  
 XX Claim 16; Fig 2A; 269pp; English.  
 XX The invention describes an isolated peptide of 100 amino acids or less in  
 CC size. The peptide is useful for treating a disease state, e.g. cancer,  
 CC arthritis, diabetes, inflammatory disease, atherosclerosis, autoimmune  
 CC disease, bacterial infection, viral infection, cardiovascular disease or  
 CC degenerative disease. This sequence represents a human targeting peptide  
 CC selective for human organs, tissues or cell types  
 XX  
 SQ Sequence 7 AA;  
 Query Match 72.7%; Score 32; DB 5; Length 7;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GGVFW 6  
 DB 2 GGIFW 6  
 |||||  
 |||||  
 RESULT 4  
 AAW69090  
 ID AAW69090 standard; peptide; 7 AA.  
 XX AC AAW69090;  
 XX  
 DT 05-OCT-1998 (first entry)  
 XX  
 DE Neuronal NOS binding peptide NBP-45.  
 XX  
 KW nNOS; neuronal nitric oxide synthase; orphan protein domain; OPD;  
 KW protein interaction network; PIN; neurological disease; therapy;  
 KW motility disorder; muscular dystrophy; amyotrophic lateral sclerosis;  
 KW Huntington's disease; Parkinson's disease; Alzheimer's disease;  
 KW Duchenne muscular dystrophy; irritable bowel syndrome.  
 XX  
 OS Synthetic.  
 XX  
 PN W09823781-A1.  
 XX  
 PD 04-JUN-1998.  
 XX  
 XX 26-NOV-1997; 97WO-US021861.  
 XX  
 XX 26-NOV-1996; 96US-0031793P.  
 PR 15-APR-1997; 97US-0043560P.  
 XX  
 XX (UYJO ) UNIV JOHNS HOPKINS.  
 XX  
 PI Li M, Stricker NL, Bredt DS, Christopherson KS;  
 XX  
 DR WPI; 1998-322754/28.  
 XX  
 XX New peptide ligands that bind specific orphan protein domains and related  
 PT nucleic acid - and methods for identifying them in random peptide  
 PT libraries, useful for treatment of neurological disease, motility  
 PT disorders and muscular dystrophy.  
 XX  
 XX Disclosure; Fig 3b; 93pp; English.  
 PS  
 XX

CC This sequence represents a neuronal nitric oxide synthase (nNOS) binding  
 CC peptide (NBP), and represents a peptide of the invention. This sequence  
 CC was identified using the method of the invention for identifying proteins  
 CC that interact with a protein binding domain (orphan protein domain, OPD)  
 CC of a first protein (protein interaction network, PIN) comprises: (a)  
 CC screening a random peptide library of transformed cells, each containing  
 CC a plasmid that includes a laco binding site, an encoding a fusion protein  
 CC (FP) of lac repressor DNA binding protein and a specific peptide (the  
 CC specific peptide being different in each cell); (b) the cells are lysed  
 CC under conditions allowing FP to remain bound to laco; (c) the FP is  
 CC contacted with OPD and plasmids encoding a peptide that binds to OPD  
 CC isolated; (d) isolated plasmids are sequenced, and nucleic acid and  
 CC protein databases scanned to identify proteins that contain the peptide.  
 CC These peptides can also be used in a peptide ligand detection system. The  
 CC peptides and peptide ligands identified by the ligand detection system,  
 CC are used for treatment of neurological disease, motility disorders or  
 CC muscular dystrophy (e.g. stroke, amyotrophic lateral sclerosis,  
 CC Huntington's, Parkinson's or Alzheimer's diseases, Duchenne muscular  
 CC dystrophy or irritable bowel syndrome). The peptides act by inhibiting  
 CC interaction between an OPD and proteins to which it normally binds, so  
 CC can also be used as reagents and as molecular labels for specific  
 CC interacting proteins, e.g. to detect nNOS  
 XX  
 SQ Sequence 7 AA;  
 Query Match 68.2%; Score 30; DB 2; Length 7;  
 Best Local Similarity 83.3%; Pred. No. 1.8e+06;  
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 GGGVFW 6  
 DB 1 GGGVDW 6  
 |||||  
 |||||  
 RESULT 5  
 AAW10773  
 ID AAW10773 standard; peptide; 7 AA.  
 XX AC AAW10773;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 10-NOV-1997 (first entry)  
 XX  
 XX Ferritin motif #16 important for selective binding affinity.  
 DE  
 XX  
 KW Functional surrogate; analyte; affinity receptor; immunoreactive group;  
 KW mimic; homogenous immunoassay; detection; diagnostic analyte; Chlamydia;  
 KW cardiac marker; tumour marker; allergen; hormone; fertility; myoglobin;  
 KW pregnancy; infectious disease; ferritin; myosin light chain; troponin;  
 KW follicle stimulating hormone; human; growth hormone; immunoglobulin E;  
 KW prolactin; parathyroid hormone; placental lactogen; hepatitis antigen;  
 KW antibody; chorionic gonadotropin; luteinising hormone; cytomegalovirus;  
 KW Streptococcus; rubella; toxoplasma; DK-MB; prostate-specific antigen;  
 KW carcinoembryonic antigen; alpha-fetoprotein; herpes virus; CA125.  
 XX  
 OS Synthetic.  
 XX  
 PN W09641172-A1.  
 XX  
 XX 19-DEC-1996.  
 PD  
 XX  
 XX 07-JUN-1996; 96WO-US010498.  
 XX  
 XX 07-JUN-1995; 95US-00476375.  
 PR  
 XX (CYTO-) CYTOGEN CORP.  
 PA  
 XX Lee-Owen FV, Carter JM;  
 PI  
 XX WPI; 1997-077284/07.  
 DR  
 XX  
 XX Labelled functional surrogate of an analyte - useful as competitor  
 PT molecule in affinity assays, esp. for detecting large macromolecules such

PT as ferritin.  
 XX Claim 56; Page 55; 156pp; English.  
 XX  
 CC This sequence represents a peptide motif derived from ferritin which is  
 CC important for selective binding affinity. Peptides containing motifs such  
 CC as this may be used as functional surrogates in the conjugate of the  
 CC invention. The novel labelled conjugate comprises at least one label  
 CC attached to a functional surrogate of an analyte of interest. The  
 CC surrogate is capable of competing effectively with the analyte for a  
 CC limiting amount of an affinity receptor for the analyte. The conjugate  
 CC exhibits an activity that is altered upon interaction with the affinity  
 CC receptor and this activity can be measured and related to the amount of  
 CC the analyte present in a sample. Functional surrogates such as this have  
 CC an immunoreactive group that allows the surrogate to compete effectively  
 CC and with the analyte for a limiting amount of its affinity receptor.  
 CC Functional surrogates are able to mimic naturally occurring analytes.  
 CC They can be labelled for use in standard competitive affinity assays  
 CC (esp. homogenous immunoassays) for detecting large macromolecules such as  
 CC polypeptides, polysaccharides, polynucleotides, glycoproteins and lipid-  
 CC containing macromolecules, as well as small haptens. Typical diagnostic  
 CC analytes for detection include cardiac or tumour markers, allergens,  
 CC hormones related to fertility-pregnancy or analytes associated with  
 CC infectious disease. In particular, the assays are useful for detecting  
 CC ferritin, follicle stimulating hormone, human growth hormone,  
 CC immunoglobulin E, prolactin, parathyroid hormone, human placental  
 CC lactogen, hepatitis antigens or antibodies against them, human chorionic  
 CC gonadotropin, human luteinising hormone, cytomegalovirus, Chlamydia,  
 CC Streptococcus a, rubella, toxoplasma, herpes virus, DK-MB, myoglobin,  
 CC myosin light chain, troponin, carcinoembryonic antigen, alpha-  
 CC fetoprotein, prostate-specific antigen and CA125 (a tumour marker).  
 CC (Updated on 25-MAR-2003 to correct PI field.)  
 XX

SQ Sequence 7 AA;

Query Match 61.4%; Score 27; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFW 6  
 || ||  
 Db 2 GGSFW 7

RESULT 6  
 AAY48924  
 ID AAY48924 standard; peptide; 7 AA.

XX AAY48924;  
 AC  
 XX  
 DT 20-MAR-2003 (revised)  
 DT 10-DEC-1999 (first entry)  
 XX  
 DE Membrane dipeptidase-binding ovary homing peptide #12.  
 XX  
 KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;  
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;  
 KW membrane dipeptidase.

XX Synthetic.  
 OS Homo sapiens.  
 XX  
 XX WO9946284-A2.

XX 16-SEP-1999.  
 XX 10-MAR-1999; 99WO-US005284.  
 XX

XX 13-MAR-1998; 98US-00042107.  
 XX 26-FEB-1999; 99US-00258754.

XX (BURN-) BURNHAM INST.

PI Rajotte D, Pasqualini R, Ruoslahti EI;  
 XX WPI; 1999-571717/48.  
 XX  
 PT New peptides which selectively home to organs or tissues, used for, e.g.  
 XX identifying target ligands and for therapy of pathological conditions.  
 XX  
 PS Example 6; Page 152; 193pp; English.

XX The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ or  
 CC tissue, for identifying a target molecule expressed by an organ or tissue  
 CC or for treating an organ or tissue pathology, where the organ or tissue  
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,  
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane  
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are  
 CC used in the exemplification of the present invention. (Updated on 20-MAR-  
 CC 2003 to correct PR field.)  
 XX

SQ Sequence 7 AA;

Query Match 61.4%; Score 27; DB 2; Length 7;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7  
 || ||  
 Db 1 GGDVWWR 7

RESULT 7  
 ADL17233  
 ID ADL17233 standard; peptide; 7 AA.

XX AC ADL17233;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 XX Phage-displayed PDZ2 and PDZ3 binding peptide SEQ ID NO:185.

XX 95 kDa post-synaptic density protein/Discs large/ZO-1 domain;  
 KW PSD-95/Discs large/ZO-1 domain; PDZ domain; fusion protein;  
 KW phage coat protein; PDZ domain binding peptide; cytostatic; nootropic;  
 KW neuroprotective; antiparkinsonian; neuroleptic; antitumour;  
 KW immunosuppressive; pulmonary; muscular; gene therapy;  
 KW Alzheimer's disease; murine typhus; chronic myeloid leukaemia;  
 KW schizophrenia; X-linked autoimmune enteropathy; tsutsugamushi disease;  
 KW facioscapulohumeral muscular dystrophy; late onset demyelinating disease;  
 KW Usher syndrome type 1; USH1; nitric oxide-mediated tissue damage; tumour;  
 KW cystic fibrosis.

XX Synthetic.  
 OS  
 XX WO2003004604-A2.

XX 16-JAN-2003.

XX 03-JUL-2002; 2002WO-US020993.

XX 06-JUL-2001; 2001US-0303634P.

XX (GETH ) GENENTECH INC.

XX Held HA, Lasky LA, Laura RP, Sidhu SS, Wong WL, Wu Y;

XX WPI; 2003-267930/26.

XX New polypeptide that interacts with a 95 kDa post-synaptic density  
 PT protein 95/Discs large/ZO-1 (PDZ) domain, useful for producing, selecting  
 PT and identifying PDZ domain binding peptides.

XX Example 3; SEQ ID NO 185; 228pp; English.

XX The present invention describes an isolated polypeptide (I) that  
 CC interacts with a 95 kDa post-synaptic density protein (PSD-95)/Discs  
 CC large/ZO-1 (PDZ) domain. Also described: (1) a fusion protein (II)  
 CC comprising a portion of a phage coat protein bonded through its carboxyl-  
 CC terminus, optionally through a peptide linker, to a PDZ domain binding  
 CC peptide, where the peptide contains 3-20 amino acid residues; (2) a  
 CC library of (II), where the fusion proteins in the library comprise a  
 CC number of PDZ domain binding peptides; (3) an assay for a PDZ domain  
 CC binding compound; (4) a polypeptide that binds to the same epitope as  
 CC (I), or that competes for binding to a PDZ domain with (I); (5) a  
 CC polynucleotide (PN) encoding (I); (6) inhibiting a polypeptide-  
 CC polypeptide interaction, by contacting a mixture comprising a first and a  
 CC second polypeptide with an inhibitor of interaction between a PDZ domain  
 CC and its ligand, where the first polypeptide comprises the PDZ domain and  
 CC the second polypeptide comprises the ligand; (7) screening for a  
 CC substance that modulates interaction between a PDZ domain polypeptide and  
 CC a molecule known to bind to the PDZ domain of the polypeptide; and (8)  
 CC screening (M) for a substance that inhibits binding of a PDZ domain  
 CC polypeptide to a molecule known to bind to the PDZ domain of the  
 CC polypeptide. (I) has cytostatic, neurotropic, neuroprotective,  
 CC antiparkinsonian, neuroleptic, antitumor, immunosuppressive, pulmonary  
 CC and muscular activities, and can be used in gene therapy. The library of  
 CC a fusion protein (II) is useful for producing a PDZ domain binding  
 CC peptide library, and for selecting PDZ domain binding peptides in  
 CC recombinant host cells. The library of (II) is also useful for  
 CC identifying a PDZ domain binding protein, by selecting PDZ domain binding  
 CC peptides using a new method. PN is useful for gene therapy, and in  
 CC diagnoses of diseases. (I) and PN are useful for treating a subject at  
 CC risk of a disorder or having a disorder associated with aberrant PDZP,  
 CC PDZD, PDZ interacting protein (PIP) or PDZ domain binding peptides (PDBP)  
 CC expression or activity such as rickettsial diseases, murine typhus,  
 CC chronic myeloid leukaemia, Alzheimer's disease, neurological disorders  
 CC such as Parkinson's disease and schizophrenia, X-linked autoimmune  
 CC enteropathy, tsutsugamushi disease, facioscapulohumeral muscular  
 CC dystrophy, late onset demyelinating disease, Usher syndrome type 1  
 CC (USH1), nitric oxide-mediated tissue damage, tumours and cystic fibrosis.  
 CC (I) is useful to identify cognate protein ligands for the PDZ domains.  
 CC Structural analysis of the peptides are useful to understand PDZ domain  
 CC structure and function, and also to identify intracellular biological  
 CC functions for these motifs and the proteins that contain them. The  
 CC peptides are further useful as PDZ domain inhibitors and are also useful  
 CC as structural models in the design of small molecule inhibitors/agonists  
 CC of the binding interaction between a PDZ domain containing protein and  
 CC its cognate ligand. The present sequence represents a peptide which is  
 CC used in the exemplification of the present invention.

XX Sequence 7 AA;

Query Match 59.1%; Score 26; DB 7; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFW 6  
 ||||  
 Db 1 GGGCSW 6

RESULT 8  
 AAW58581  
 ID AAW58581 standard; peptide; 5 AA.

XX AAW58581;

XX 17-OCT-2003 (revised)  
 DT 07-SEP-1998 (first entry)

DE Kojibiose phosphorylase peptide 357-361.

KW Kojibiose phosphorylase; Thermoanaerobium brockii; TKP1; hydrolyse;  
 KW saccharide; beta-D-glucose-1-phosphoric acid; sweetener; stabiliser;  
 KW pharmaceutical; food; cosmetic; thermostable.

OS Thermoanaerobacter brockii.  
 XX EP841398-A2.  
 XX 13-MAY-1998.  
 PD 07-NOV-1997; 97BP-00308981.  
 FF 08-NOV-1996; 96JP-00311235.  
 PR 03-MAR-1997; 97JP-00061710.  
 XX (HAYB ) HAYASHIBARA SEIBUTSU KAGAKU.  
 PA Nishimoto T, Kubota M, Chaen H, Miyake T;  
 XX WPI; 1998-252942/23.  
 DR New kojibiose phosphorylase, especially from Thermoanaerobium - used to  
 XX produce saccharide compositions, used as e.g. sweeteners or stabilisers  
 PT in pharmaceuticals, foods and cosmetics.  
 XX Claim 4; Page 33; 42pp; English.

XX The present sequence represents a kojibiose phosphorylase peptide from  
 CC Thermoanaerobium brockii. Kojibiose phosphorylase hydrolyses kojibiose in  
 CC the presence of inorganic phosphate (Pi) and/or its salt to form D-  
 CC glucose and beta-D-glucose-1-phosphoric acid and/or its salt. Saccharide  
 CC compositions, containing a D-glucosyl-transferred saccharide, are used in  
 CC e.g., foods, animal feeds, beverages, cosmetics, pharmaceuticals or  
 CC tobacco as sweeteners, taste improvers, osmosis regulators, glossing  
 CC agents, crystallisation inhibitors, anti-carries agents, growth promoters  
 CC for bifid bacteria and promoters of mineral absorption. They may also be  
 CC used to stabilise pharmaceuticals e.g. cytokines, hormones, vaccines,  
 CC antibiotics, enzymes and microorganisms. Kojibiose phosphorylase is used  
 CC to produce kojibiose by contacting, in the presence of Pi, with maltose  
 CC and maltose phosphorylase (MP) on maltose or trehalose phosphorylase (TP)  
 CC on trehalose. The saccharide compositions have a sweetness which  
 CC harmonises with substances which are sour, bitter, acidic, salty,  
 CC astringent and delicious and is acid and heat tolerant. The high thermal  
 CC stability of kojibiose phosphorylase makes possible large scale,  
 CC relatively inexpensive production of D-glucosyl transferred saccharides  
 CC which are normally difficult to produce. (Updated on 17-OCT-2003 to  
 CC standardise OS field)

XX Sequence 5 AA;

Query Match 56.8%; Score 25; DB 2; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
 ||||  
 Db 1 GHVFW 5

RESULT 9  
 AAW39859  
 ID AAW39859 standard; peptide; 7 AA.

XX AAW39859;

XX 16-JUN-1998 (first entry)

DT Heavy chain CDR3 of catalytic antibody 19G8.

XX Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX Mus sp.

XX WO9749800-A1.

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XX PD 31-DEC-1997.
XX PF
XX PR 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 4; Page 92; 147pp; English.
XX SQ AAW39857-59 represent the sequences of the heavy chain complementarity
CC determining regions (CDRs) of the catalytic antibody 19G8, which is able
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. The 19G8 antibody was identified
CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC transition state analogue. Antibody 19G8 has a per minute Kcat of 0.091.
CC The antibodies reduce the concentration of cocaine in a subject, and are
CC used particularly for the treatment of an overdose. They are also used
CC for treating addiction (by reducing the in vivo concentration that can be
CC achieved)
XX SQ Sequence 7 AA;
Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGVF 5
DB |||:|
1 GGGLF 5
RESULT 10
AAW39874
ID AAW39874 standard; peptide; 7 AA.
XX AC AAW39874;
XX DT 16-JUN-1998 (first entry)
XX DE Heavy chain CDR3 of a catalytic antibody capable of degrading cocaine.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addition.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 4; Page 92; 147pp; English.
XX SQ AAW39857-59 represent the sequences of the heavy chain complementarity
CC determining regions (CDRs) of the catalytic antibody 19G8, which is able
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. The 19G8 antibody was identified
CC using TSA1, which is an immunogenic conjugate of a phosphate monoester
CC transition state analogue. Antibody 19G8 has a per minute Kcat of 0.091.
CC The antibodies reduce the concentration of cocaine in a subject, and are
CC used particularly for the treatment of an overdose. They are also used
CC for treating addiction (by reducing the in vivo concentration that can be
CC achieved)
XX SQ Sequence 7 AA;
Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGVF 5
DB |||:|
1 GGGLF 5
RESULT 11
AAW39862
ID AAW39862 standard; peptide; 7 AA.
XX AC AAW39862;
XX DT 16-JUN-1998 (first entry)
XX DE Heavy chain CDR3 of catalytic antibody 15A10.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addition.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 2; Page 93; 147pp; English.
XX SQ AAW39860-62 represent the sequences of the heavy chain complementarity
CC determining regions (CDRs) of the catalytic antibody 15A10, which is able
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)

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XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 1; Page 5; 147pp; English.
XX SQ AAW39872-74 represent the sequences of the heavy chain complementarity
CC determining regions (CDRs) of a catalytic antibody which is capable of
CC degrading cocaine. A series of cocaine transition state analogues (TSAs)
CC were prepared and used to immunise mice for production of hybridomas.
CC Catalytic antibodies were identified by their capacity to release 3H-
CC benzoic acid from 3H-phenyl cocaine. These antibodies were found to have
CC CDRs of the present sequence. The antibodies reduce the concentration of
CC cocaine in a subject, and are used particularly for the treatment of an
CC overdose. They are also used for treating addiction (by reducing the in
CC vivo concentration that can be achieved)
XX SQ Sequence 7 AA;
Query Match 56.8%; Score 25; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 1 GGGVF 5
DB |||:|
1 GGGLF 5
RESULT 11
AAW39862
ID AAW39862 standard; peptide; 7 AA.
XX AC AAW39862;
XX DT 16-JUN-1998 (first entry)
XX DE Heavy chain CDR3 of catalytic antibody 15A10.
XX KW Variable domain; lambda light chain; catalytic antibody; degradation;
XX KW cocaine; cocaine transition state analogue; TSA; benzoic acid;
XX KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;
XX KW overdose; addition.
XX OS Mus sp.
XX PN WO9749800-A1.
XX PD 31-DEC-1997.
XX PF 25-JUN-1997; 97WO-US010965.
XX PR 25-JUN-1996; 96US-00672345.
XX PA (UYCO ) UNIV COLUMBIA NEW YORK.
XX PI Landry DW;
XX DR WPI; 1998-077166/07.
XX PT New catalytic antibodies able to decompose cocaine, single-chain
XX PT analogues - used to treat cocaine overdose and addiction, required in far
XX PT smaller doses than antibodies that antagonise cocaine by simply binding.
XX PS Claim 2; Page 93; 147pp; English.
XX SQ AAW39860-62 represent the sequences of the heavy chain complementarity
CC determining regions (CDRs) of the catalytic antibody 15A10, which is able
CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)

```

CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 15A10 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 15A10 has a per minute Kcat of 2.3.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)  
 CC  
 XX

SQ Sequence 7 AA;

Query Match 56.8%; Score 25; DB 2; Length 7;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5  
 |||:  
 Db 1 GGGLF 5

RESULT 12

AAW39856  
 ID AAW39856 standard; peptide; 7 AA.

XX

AC AAW39856;

XX

DT 16-JUN-1998 (first entry)

XX

DE Heavy chain CDR3 of catalytic antibody 9A3.

XX

KW Variable domain; lambda light chain; catalytic antibody; degradation;  
 KW cocaine; cocaine transition state analogue; TSA; benzoic acid;  
 KW phenyl cocaine; immunogenic conjugate; reduction; cocaine; treatment;  
 KW overdose; addiction.

XX

OS Mus sp.

XX

PN WO9749800-A1.

XX

PD 31-DEC-1997.

XX

PF 25-JUN-1997; 97WO-US010965.

XX

PR 25-JUN-1996; 96US-00672345.

XX

PA (UYCO ) UNIV COLUMBIA NEW YORK.

XX

PI Landry DW;

XX

DR WPI; 1998-077166/07.

XX

PT New catalytic antibodies able to decompose cocaine, single-chain  
 PT analogues - used to treat cocaine overdose and addiction, required in far  
 PT smaller doses than antibodies that antagonise cocaine by simply binding.

XX

PS Claim 6; Page 91; 147pp; English.

XX

AAW39854-56 represent the sequences of the heavy chain complementarity  
 determining regions (CDRs) of the catalytic antibody 9A3, which is able  
 CC to degrade cocaine. A series of cocaine transition state analogues (TSAs)  
 CC were prepared and used to immunise mice for production of hybridomas.  
 CC Catalytic antibodies were identified by their capacity to release 3H-  
 CC benzoic acid from 3H-phenyl cocaine. The 9A3 antibody was identified  
 CC using TSA1, which is an immunogenic conjugate of a phosphate monoester  
 CC transition state analogue. Antibody 9A3 has a per minute Kcat of 0.015.  
 CC The antibodies reduce the concentration of cocaine in a subject, and are  
 CC used particularly for the treatment of an overdose. They are also used  
 CC for treating addiction (by reducing the in vivo concentration that can be  
 CC achieved)  
 CC

SQ Sequence 7 AA;

RESULT 14

AAU81231

ID AAU81231 standard; peptide; 7 AA.

XX

Query Match 56.8%; Score 25; DB 2; Length 7;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5  
 |||:  
 Db 1 GGGLF 5

RESULT 13

AAW40897

ID AAW40897 standard; peptide; 7 AA.

XX

AC AAW40897;

XX

DT 27-AUG-2003 (revised)

XX

DT 09-JUN-1998 (first entry)

XX

DE Leader sequence 16, development of substances against Bundyviridae.

XX

KW Virus inhibitory peptide; inhibition; ligand library;  
 KW competitive affinity-elution; prophylactic substance;  
 KW combinatorial therapy; pathogen diagnosis; leader molecule.

XX

OS Bunyaviridae.

XX

PN WO9745743-A1.

XX

PD 04-DEC-1997.

XX

PF 30-MAY-1997; 97WO-FI000339.

XX

PR 30-MAY-1996; 96FI-00002269.

XX

PA (UYHE-) UNIV HELSINKI LICENSING LTD.

XX

PI Lankinen H, Heiskanen T, Vaheri A, Lundkvist A;

XX

DR WPI; 1998-032807/03.

XX

PT Selection of target pathogen inhibiting substances - useful for  
 PT comparative drug design to provide therapeutically active, protective and  
 PT prophylactic substances.

XX

PS Claim 14; Page 68; 81pp; English.

XX

CC This is a peptide which is useful as a leader molecule. It is used for  
 CC the development of substances active against enveloped pathogens such as  
 CC viruses from the family Bunyaviridae. Its selection involved the  
 CC reaction of a ligand library with the bound target pathogen and the  
 CC pathogen bound ligands are subjected to competitive affinity-elution with  
 CC at least one neutralising substance. The method is useful for comparative  
 CC drug design to provide therapeutically active, protective and/or  
 CC prophylactic substances and developing combinatorial therapies as well as  
 CC for pathogen diagnostics. The method also identifies "leader molecules",  
 CC which not only have great affinity, but also mimic the functions of known  
 CC neutralising substances. (Updated on 27-AUG-2003 to correct OS field.)  
 CC

SQ Sequence 7 AA;

Query Match 56.8%; Score 25; DB 2; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VFWQ 7  
 |||:  
 Db 3 IFWQ 6

AAU81231;  
 09-APR-2002 (first entry)  
 Human trkC antibody heavy chain CDR1 of variable region #1.  
 Human; mouse; anti-trkC agonist monoclonal antibody; trkC; antibody;  
 trkA; trkB; cisplatin-induced neuropathy; pyridoxine-induced neuropathy;  
 peripheral neuropathy; diabetic neuropathy; neurodegenerative disease;  
 large-fibre sensory neuropathy; amyotrophic lateral sclerosis; tumour;  
 nerve cell injury; blood cell disorder; leukopaenia; eosinopaenia; wound;  
 basopaenia; lymphopaenia; monocytopenia; neutropaenia; cancer; ulcer;  
 Alzheimer's disease; Parkinson's disease; Huntington's disease; diabetes;  
 sickle cell disease; cardiac ischaemia; cerebrovascular disorder;  
 cellular degeneration; gene therapy.  
 Homo sapiens.  
 WO200198361-A2.  
 27-DEC-2001.  
 22-JUN-2001; 2001WO-US020153.  
 22-JUN-2000; 2000US-0213141P.  
 05-OCT-2000; 2000US-0238319P.  
 (GETH ) GENENTECH INC.  
 Devaux B, Hongo JS, Presta LG, Shelton DL;  
 WPI; 2002-130790/17.  
 Novel anti-trkC agonist monoclonal antibody useful for treating  
 neurodegenerative disease, shows no significant cross-reactivity with  
 trkA/trkB, and recognizes epitope in domain 5 of trkC.  
 Claim 12; Fig 11; 121pp; English.  
 The invention relates to an anti-trkC agonist monoclonal antibody which  
 shows no significant cross-reactivity with trkA or trkB, and recognizes  
 an epitope in domain 5 of trkC. The antibodies of the invention are  
 effective in the treatment of cisplatin- or pyridoxine-induced  
 neuropathy, peripheral neuropathy, diabetic neuropathy and large-fibre  
 sensory neuropathy, neurodegenerative disease including amyotrophic  
 lateral sclerosis, nerve cell injuries, disorders of insufficient blood  
 cells such as leukopaenia including eosinopaenia, basopaenia,  
 lymphopaenia, monocytopenia, neutropaenia, Alzheimer's disease,  
 Parkinson's disease, Huntington's disease and tumours. The sequences are  
 also useful for inducing angiogenesis for treating wounds, ulcers and  
 diabetic complications of sickle cell disease, for treating cardiac  
 ischaemia and cerebrovascular disorders and in the diagnosis of diseases  
 involving cellular degeneration. Sequences AAU81229-AAU81284 represent  
 human and mouse anti-trkC agonist monoclonal antibodies and antibody  
 fragments of the invention

Sequence 7 AA;

Query Match 56.8%; Score 25; DB 5; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
 || : |  
 Db 2 GGYW 6

RESULT 15  
 AAU86976  
 ID AAU86976 standard; peptide; 5 AA.  
 XX  
 AC AAU86976;  
 XX

21-MAY-2002 (first entry)  
 Estradiol mimotope peptide #24.  
 Estradiol; mimotope; estrone-3-glucuronide; steroid detection;  
 immunoassay; phage display; immunogen.  
 Synthetic.  
 WO200212270-A1.  
 14-FEB-2002.  
 26-JUL-2001; 2001WO-EP008705.  
 03-AUG-2000; 2000EP-00306613.  
 (UNIL ) UNILEVER PLC.  
 (UNIL ) UNILEVER NV.  
 (UNIL ) HINDUSTAN LEVER LTD.  
 Badley RA, Berry MJ, Williams SC;  
 WPI; 2002-241729/29.  
 Peptide mimotope capable of binding specifically to antibody specific to  
 estradiol, useful for assaying presence and/or amount of estradiol,  
 especially estrone-3-glucuronide in sample.  
 Claim 3; Page 22; 57pp; English.  
 The invention relates to a purified peptide mimotope capable of binding  
 specifically to an antibody specific to estradiol. Also included are a  
 solid support having immobilised (releasably or non-releasably) peptide  
 mimotopes, an immunoassay test device for the detection of estradiol in  
 the sample, comprising the mimotopes and an antibody capable of binding  
 specifically to the mimotopes to generate a detectable signal and an  
 isolated nucleic acid encoding the peptide mimotopes. The mimotope is  
 useful for assaying the presence and/or amount of estradiol preferably  
 estrone-3-glucuronide in a sample which is urine or serum sample to be  
 tested and is also utilised in an immunoassay test device, and further  
 can be used as immunogens. The mimotope be used to construct new, or  
 improve the performance of old, immunoassay test formats and devices.  
 They can, for example, be utilised essentially to tune the signal in  
 conventional displacement assays for the detection of estradiol. The  
 mimotope can be bound directly to certain assay surfaces which are  
 otherwise non-compatible with estradiol on such surfaces needing to be  
 bound to the surface by complexing with another - often proteinaceous -  
 molecule. The mimotope is capable of being bound to the antigen-binding  
 site of an antibody in a selective fashion in the presence of excess  
 quantities of other undesired materials, and tightly enough (i.e. with  
 high enough affinity) that when used in an immunoassay, it provides a  
 useful result. The present sequence is a peptide mimotopes of the  
 invention

Sequence 5 AA;

Query Match 54.5%; Score 24; DB 5; Length 5;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GVPW 6  
 | : |  
 Db 1 GLFW 4

Search completed: August 3, 2005, 12:03:06  
 Job time : 100.333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 25 Seconds  
(without alignments)

20.902 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 61165

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*

4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*

5: /cgn2\_6/ptodata/1/iaa/PCTUS COMB.pep.\*

6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	44	100.0	7	3	US-09-326-718-2
2	27	61.4	7	3	US-09-258-754-300
3	27	61.4	7	3	US-09-042-107-300
4	27	61.4	7	4	US-09-722-250D-300
5	27	61.4	7	4	US-09-676-475A-300
6	25	56.8	5	2	US-08-966-388-3
7	25	56.8	5	3	US-09-188-403-3
8	25	56.8	5	3	US-09-188-404-3
9	25	56.8	5	3	US-08-281-259-3
10	25	56.8	7	2	US-08-672-345C-60
11	25	56.8	7	2	US-08-672-345C-63
12	25	56.8	7	2	US-08-672-345C-66
13	25	56.8	7	2	US-08-672-345C-78
14	25	56.8	7	3	US-09-214-095D-60
15	25	56.8	7	3	US-09-214-095D-63
16	25	56.8	7	3	US-09-214-095D-66
17	25	56.8	7	3	US-09-214-095D-78
18	24	54.5	7	4	US-09-731-242A-49
19	23	52.3	7	4	US-09-388-788-2
20	23	52.3	7	4	US-09-731-242A-53
21	22	50.0	5	1	US-07-969-307A-6
22	22	50.0	5	2	US-08-868-497-8
23	22	50.0	5	3	US-08-860-808E-14
24	22	50.0	5	3	US-08-860-808E-24
25	22	50.0	5	3	US-09-362-230-8
26	22	50.0	5	5	PCT-US94-07926-8
27	22	50.0	6	1	US-08-375-911A-8

28	50.0	6	3	US-08-860-808E-4	Sequence 4, Appli
29	50.0	6	3	US-08-860-808E-8	Sequence 8, Appli
30	50.0	6	3	US-08-860-808E-9	Sequence 9, Appli
31	50.0	6	4	US-08-940-136-272	Sequence 272, App
32	50.0	6	4	US-08-877-605-272	Sequence 272, App
33	50.0	6	4	US-08-877-605-314	Sequence 314, App
34	50.0	6	4	US-08-877-605-323	Sequence 323, App
35	50.0	6	4	US-08-877-605-331	Sequence 331, App
36	50.0	6	4	US-09-913-763-1	Sequence 1, Appli
37	50.0	7	3	US-09-258-754-384	Sequence 384, App
38	50.0	7	3	US-09-042-107-384	Sequence 384, App
39	50.0	7	4	US-08-877-605-337	Sequence 337, App
40	50.0	7	4	US-09-722-250D-384	Sequence 384, App
41	50.0	7	4	US-09-676-475A-384	Sequence 384, App
42	47.7	6	1	US-07-596-867C-9	Sequence 9, Appli
43	47.7	6	1	US-08-167-939A-9	Sequence 9, Appli
44	47.7	6	1	US-08-567-538-9	Sequence 9, Appli
45	47.7	6	2	US-08-482-228-8	Sequence 8, Appli
46	47.7	6	3	US-08-482-528-8	Sequence 8, Appli
47	47.7	6	4	US-09-461-325-278	Sequence 278, App
48	47.7	6	4	US-09-302-357-65	Sequence 65, Appl
49	47.7	6	4	US-08-877-605-291	Sequence 291, App
50	47.7	6	4	US-10-012-542-278	Sequence 278, App
51	47.7	6	4	US-10-115-123-278	Sequence 278, App
52	47.7	6	5	PCT-US91-07715A-9	Sequence 9, Appli
53	47.7	7	1	US-07-969-307A-14	Sequence 14, Appl
54	47.7	7	1	US-08-192-300-10	Sequence 10, Appl
55	47.7	7	4	US-08-877-605-273	Sequence 273, App
56	45.5	6	1	US-07-973-235A-12	Sequence 12, Appl
57	45.5	6	1	US-07-973-235A-13	Sequence 13, Appl
58	45.5	6	1	US-07-973-235A-24	Sequence 24, Appl
59	45.5	6	2	US-08-462-720-12	Sequence 12, Appl
60	45.5	6	2	US-08-462-720-13	Sequence 13, Appl
61	45.5	6	2	US-08-462-720-24	Sequence 24, Appl
62	45.5	7	1	US-07-956-700B-71	Sequence 71, Appl
63	45.5	7	1	US-08-476-537-71	Sequence 71, Appl
64	45.5	7	1	US-08-485-607-71	Sequence 71, Appl
65	45.5	7	2	US-08-475-879-71	Sequence 71, Appl
66	45.5	7	3	US-09-433-043B-71	Sequence 71, Appl
67	45.5	7	4	US-09-756-223A-10	Sequence 10, Appl
68	45.5	7	4	US-09-731-242A-48	Sequence 48, Appl
69	43.2	4	1	US-07-802-667-8	Sequence 8, Appli
70	43.2	4	1	US-07-802-667-11	Sequence 11, Appl
71	43.2	5	1	US-07-969-307A-7	Sequence 7, Appli
72	43.2	5	3	US-09-091-814-64	Sequence 64, Appl
73	43.2	5	4	US-09-376-463-12	Sequence 12, Appl
74	43.2	5	6	5217869-11	Patent No. 5217869
75	43.2	5	6	5217869-11	Patent No. 5217869
76	43.2	6	1	US-07-969-307A-12	Sequence 12, Appl
77	43.2	6	1	US-07-973-235A-18	Sequence 18, Appl
78	43.2	6	1	US-07-802-667-32	Sequence 32, Appl
79	43.2	6	1	US-08-375-911A-7	Sequence 7, Appli
80	43.2	6	2	US-08-462-720-18	Sequence 18, Appl
81	43.2	6	3	US-08-115-753-8	Sequence 8, Appli
82	43.2	6	3	US-08-635-928-2	Sequence 2, Appli
83	43.2	6	3	US-08-635-928-3	Sequence 3, Appli
84	43.2	7	1	US-07-968-781A-83	Sequence 83, Appl
85	43.2	7	1	US-07-969-307A-16	Sequence 16, Appl
86	43.2	7	1	US-08-062-024B-1	Sequence 1, Appli
87	43.2	7	1	US-08-325-562-3	Sequence 3, Appli
88	43.2	7	1	US-08-437-795-3	Sequence 3, Appli
89	43.2	7	2	US-08-540-406-13	Sequence 13, Appl
90	43.2	7	2	US-08-756-407-1	Sequence 1, Appli
91	43.2	7	2	US-08-637-759B-134	Sequence 134, App
92	43.2	7	3	US-08-871-355A-134	Sequence 134, App
93	43.2	7	3	US-08-656-055-13	Sequence 13, Appl
94	43.2	7	3	US-08-954-668-13	Sequence 13, Appl
95	43.2	7	3	US-09-201-945-134	Sequence 134, App
96	43.2	7	4	US-08-918-658-13	Sequence 13, Appl
97	43.2	7	4	US-09-724-631-13	Sequence 13, Appl
98	43.2	7	4	US-08-877-605-266	Sequence 266, App
99	43.2	7	4	US-08-954-701A-13	Sequence 13, Appl
100	43.2	7	4	US-09-192-854-5	Sequence 5, Appli

## ALIGNMENTS

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RESULT 1
US-09-326-718-2
; Sequence 2, Application US/09326718
; Patent No. 6303573
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Mackenna, Deidre A.
; TITLE OF INVENTION: Heart Homing Peptides and Methods of
; TITLE OF INVENTION: Using Same
; FILE REFERENCE: P-LJ 3512
; CURRENT APPLICATION NUMBER: US/09/326,718
; CURRENT FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-326-718-2

Query Match      100.0%; Score 44; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 GGGVFWQ 7
Db      1 GGGVFWQ 7
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RESULT 2
US-09-258-754-300
; Sequence 300, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LJ 3443
; CURRENT APPLICATION NUMBER: US/09/258,754
; CURRENT FILING DATE: 1999-02-26
; EARLIER APPLICATION NUMBER: 09/042,107
; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 300
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-300

Query Match      61.4%; Score 27; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGVFWQ 7
Db      1 GGDVWNR 7
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RESULT 3
US-09-042-107-300
; Sequence 300, Application US/09042107
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; Patent No. 6232287
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 2892
; CURRENT APPLICATION NUMBER: US/09/042,107
; CURRENT FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 436
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 300
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-042-107-300

Query Match      61.4%; Score 27; DB 3; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGVFWQ 7
Db      1 GGDVWNR 7
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RESULT 4
US-09-722-250D-300
; Sequence 300, Application US/09722250D
; Patent No. 6610651
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 300
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-300

Query Match      61.4%; Score 27; DB 4; Length 7;
Best Local Similarity 57.1%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 GGGVFWQ 7
Db      1 GGDVWNR 7
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RESULT 5
US-09-676-475A-300
; Sequence 300, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A
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; CURRENT FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 09/042,107  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: Patent In Ver. 2.0  
; SEQ ID NO 300  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-676-475A-300

Query Match 61.4%; Score 27; DB 4; Length 7;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 GGGVFWQ 7  
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Db 1 GGDVWVR 7

RESULT 6  
US-08-966-388-3  
; Sequence 3, Application US/08966388  
; Patent No. 5965412  
; GENERAL INFORMATION:  
; APPLICANT: Tomoyuki NISHIMOTO  
; APPLICANT: Michio KUBOTA  
; APPLICANT: Hiroto CHAEN  
; APPLICANT: Toshio MIYAKE  
; TITLE OF INVENTION: KOJIBIOSE-PHOSPHORYLASE, ITS PREPARATION AND USES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/966,388  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 311,235/1996  
; FILING DATE: 8-NOV-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 61,710/97  
; FILING DATE: 3-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal fragment  
US-08-966-388-3

Query Match 56.8%; Score 25; DB 2; Length 5;

Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GGVFW 6  
|  
Db 1 GHVFW 5

RESULT 7  
US-09-188-403-3  
; Sequence 3, Application US/09188403  
; Patent No. 6066477  
; GENERAL INFORMATION:  
; APPLICANT: Tomoyuki NISHIMOTO  
; APPLICANT: Michio KUBOTA  
; APPLICANT: Hiroto CHAEN  
; APPLICANT: Toshio MIYAKE  
; TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NEIMARK  
; STREET: 419 Seventh Street, N.W., Suite 300  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/188,403  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/966,388  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 61,710/97  
; FILING DATE: 3-MAR-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROWDY, Roger L.  
; REGISTRATION NUMBER: 25,618  
; REFERENCE/DOCKET NUMBER:  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 5 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; FRAGMENT TYPE: internal fragment  
US-09-188-403-3

Query Match 56.8%; Score 25; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
|  
Db 1 GHVFW 5

RESULT 8  
US-09-188-404-3  
; Sequence 3, Application US/09188404  
; Patent No. 6140487  
; GENERAL INFORMATION:  
; APPLICANT: Tomoyuki NISHIMOTO

APPLICANT: Michio KUBOTA  
APPLICANT: Hitoto CHAEN  
APPLICANT: Toshio MIYAKE  
TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/188,404  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/966,388  
FILING DATE:  
FILING DATE: 3-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
US-09-188-404-3

Query Match 56.8%; Score 25; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
Db 1 GHVFW 5

RESULT 9  
US-09-281-259-3  
Sequence 3, Application US/09281259  
Patent No. 6204377  
GENERAL INFORMATION:  
APPLICANT: Tomoyuki NISHIMOTO  
APPLICANT: Michio KUBOTA  
APPLICANT: Hitoto CHAEN  
APPLICANT: Toshio MIYAKE  
TITLE OF INVENTION: KOJIBIOSE PHOSPHORYLASE, ITS PREPARATION AND USES  
NUMBER OF SEQUENCES: 10  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BROWDY AND NEIMARK  
STREET: 419 Seventh Street, N.W., Suite 300  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/281,259  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/966,388  
FILING DATE:  
FILING DATE: 3-MAR-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: BROWDY, Roger L.  
REGISTRATION NUMBER: 25,618  
REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202-628-5197  
TELEFAX: 202-737-3528  
TELEX: 248633  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 5 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
FRAGMENT TYPE: internal fragment  
US-09-281-259-3

Query Match 56.8%; Score 25; DB 3; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
Db 1 GHVFW 5

RESULT 10  
US-08-672-345C-60  
Sequence 60, Application US/08672345C  
Patent No. 5948658  
GENERAL INFORMATION:  
APPLICANT: Landry Donald, W.  
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
NUMBER OF SEQUENCES: 108  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Cooper and Dunham LLP  
STREET: 1185 Avenue of the Americas  
CITY: New York  
STATE: New York  
COUNTRY: USA  
ZIP: 10036  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/672,345C  
FILING DATE: 24-JUN-1996  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: White, John P.  
REGISTRATION NUMBER: 28,678  
REFERENCE/DOCKET NUMBER: 0575/51400  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212-278-0400  
TELEFAX: 212-391-0525  
INFORMATION FOR SEQ ID NO: 60:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids

;  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-60  
  
Query Match 56.8%; Score 25; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 GGGVF 5  
|||:  
Db 1 GGGLF 5

RESULT 11  
US-08-672-345C-63  
; Sequence 63, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 63:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-63

Query Match 56.8%; Score 25; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5  
|||:  
Db 1 GGGLF 5

RESULT 12  
US-08-672-345C-66  
; Sequence 66, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:

;  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 66:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-66

Query Match 56.8%; Score 25; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGGVF 5  
|||:  
Db 1 GGGLF 5

RESULT 13  
US-08-672-345C-78  
; Sequence 78, Application US/08672345C  
; Patent No. 5948658  
; GENERAL INFORMATION:  
; APPLICANT: Landry Donald, W.  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; NUMBER OF SEQUENCES: 108  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Cooper and Dunham LLP  
; STREET: 1185 Avenue of the Americas  
; CITY: New York  
; STATE: New York  
; COUNTRY: USA  
; ZIP: 10036  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/672,345C  
; FILING DATE: 24-JUN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: White, John P.  
; REGISTRATION NUMBER: 28,678  
; REFERENCE/DOCKET NUMBER: 0575/51400  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-278-0400  
; TELEFAX: 212-391-0525  
; INFORMATION FOR SEQ ID NO: 78:  
; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-672-345C-78

Query Match 56.8%; Score 25; DB 2; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGVF 5  
| | | : |  
Db 1 GGGLF 5

## RESULT 14

US-09-214-095D-60  
; Sequence 60, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 60  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-60

Query Match 56.8%; Score 25; DB 3; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGVF 5  
| | | : |  
Db 1 GGGLF 5

## RESULT 15

US-09-214-095D-63  
; Sequence 63, Application US/09214095D  
; Patent No. 6280987  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 51400-A-PCT-US  
; CURRENT APPLICATION NUMBER: US/09/214,095D  
; CURRENT FILING DATE: 1999-07-19  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.0  
; SEQ ID NO 63  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Murinae gen. sp.  
US-09-214-095D-63

Query Match 56.8%; Score 25; DB 3; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGVF 5  
| | | : |  
Db 1 GGGLF 5

Search completed: August 3, 2005, 11:58:08  
Job time : 26 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 11:57:01 ; Search time 89.3333 Seconds  
(without alignments)  
30.529 Million cell updates/sec

Title: US-09-910-582B-2

Perfect score: 44

Sequence: 1 GGGVFWQ 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 71902

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

#### Database :

Published Applications AA:\*  
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2: /cgn2\_6/ptodata/2/pubpaa/PCT\_NEW\_PUB.pep.\*  
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21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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1	44	100.0	7	9	US-09-782-650-1
2	44	100.0	7	10	US-09-910-582B-2
3	44	100.0	7	17	US-10-838-289-34
4	27	61.4	7	17	US-10-838-289-100
5	27	61.4	7	17	US-10-607-595-300
6	26	59.1	7	14	US-10-190-082-185
7	25	56.8	7	10	US-09-940-727B-60
8	25	56.8	7	10	US-09-940-727B-63
9	25	56.8	7	10	US-09-940-727B-66
10	25	56.8	7	10	US-09-940-727B-78
11	25	56.8	7	16	US-10-312-316-3
					Sequence 1, Appli
					Sequence 2, Appli
					Sequence 34, Appl
					Sequence 100, App
					Sequence 300, App
					Sequence 185, App
					Sequence 60, Appl
					Sequence 63, Appl
					Sequence 66, Appl
					Sequence 78, Appl
					Sequence 3, Appli

25	56.8	7	17	US-10-893-576-95	Sequence 95, Appl
25	56.8	7	17	US-10-893-576-98	Sequence 98, Appl
25	56.8	7	18	US-10-984-960A-22	Sequence 22, Appl
25	56.8	7	18	US-10-984-960A-77	Sequence 77, Appl
24	54.5	5	11	US-09-920-306-27	Sequence 27, Appl
24	54.5	6	14	US-10-285-045-30	Sequence 30, Appl
24	54.5	6	14	US-10-284-660-30	Sequence 30, Appl
24	54.5	6	15	US-10-306-631-70	Sequence 70, Appl
24	54.5	6	16	US-10-807-635-30	Sequence 30, Appl
24	54.5	6	17	US-10-936-138-30	Sequence 30, Appl
24	54.5	6	18	US-10-496-869-3	Sequence 3, Appli
24	54.5	7	9	US-09-731-242A-49	Sequence 49, Appl
24	54.5	7	18	US-10-783-786-49	Sequence 49, Appl
25	52.3	6	9	US-09-740-026A-28	Sequence 28, Appl
26	52.3	7	9	US-09-731-242A-53	Sequence 53, Appl
27	52.3	7	14	US-10-190-082-61	Sequence 61, Appl
28	52.3	7	14	US-10-277-217-7	Sequence 7, Appli
29	52.3	7	18	US-10-783-786-53	Sequence 53, Appl
30	50.0	5	15	US-10-359-363A-44	Sequence 44, Appl
31	50.0	5	15	US-10-359-363A-45	Sequence 45, Appl
32	50.0	5	18	US-10-887-775-21	Sequence 21, Appl
33	50.0	6	15	US-10-283-599-272	Sequence 272, App
34	50.0	6	15	US-10-359-363A-39	Sequence 39, Appl
35	50.0	6	15	US-10-359-363A-101	Sequence 101, App
36	50.0	6	16	US-10-848-750-1	Sequence 1, Appli
37	50.0	6	17	US-10-829-388-18	Sequence 18, Appl
38	50.0	6	17	US-10-735-916A-8	Sequence 8, Appli
39	50.0	6	18	US-10-887-775-20	Sequence 20, Appl
40	50.0	6	18	US-10-991-217-272	Sequence 272, App
41	50.0	7	14	US-10-220-033-21	Sequence 21, Appl
42	50.0	7	15	US-10-359-363A-38	Sequence 38, Appl
43	50.0	7	15	US-10-413-943-40	Sequence 40, Appl
44	50.0	7	17	US-10-607-595-384	Sequence 384, App
45	50.0	7	18	US-10-887-775-19	Sequence 19, Appl
46	47.7	4	9	US-09-211-691-18	Sequence 18, Appl
47	47.7	4	14	US-10-317-773-18	Sequence 18, Appl
48	47.7	5	17	US-10-317-428-18	Sequence 3, Appli
49	47.7	5	17	US-10-923-257-3	Sequence 5, Appli
50	47.7	6	9	US-09-867-847-52	Sequence 52, Appl
51	47.7	6	14	US-10-012-542-278	Sequence 278, App
52	47.7	6	14	US-10-115-123-278	Sequence 278, App
53	47.7	6	14	US-10-190-082-667	Sequence 667, App
54	47.7	6	17	US-10-825-958-50	Sequence 50, Appl
55	47.7	6	18	US-10-800-834-278	Sequence 278, App
56	47.7	7	9	US-09-205-658-296	Sequence 296, App
57	47.7	7	9	US-09-828-708-20	Sequence 20, Appl
58	47.7	7	10	US-09-791-153A-20	Sequence 20, Appl
59	47.7	7	10	US-09-963-693-296	Sequence 296, App
60	47.7	7	17	US-10-630-009-20	Sequence 20, Appl
61	47.7	7	17	US-10-400-991-47	Sequence 47, Appl
62	45.5	5	15	US-10-367-654-196	Sequence 3, Appli
63	45.5	6	10	US-09-912-414-3	Sequence 41, Appl
64	45.5	6	10	US-09-800-187-41	Sequence 41, Appl
65	45.5	6	15	US-10-414-524-68	Sequence 68, Appl
66	45.5	6	17	US-10-808-187-1752	Sequence 1752, Ap
67	45.5	6	17	US-10-658-232-18	Sequence 18, Appl
68	45.5	7	9	US-09-731-242A-48	Sequence 48, Appl
69	45.5	7	10	US-09-372-656-41	Sequence 41, Appl
70	45.5	7	14	US-10-015-979-79	Sequence 79, Appl
71	45.5	7	14	US-10-190-082-11	Sequence 11, Appl
72	45.5	7	14	US-10-190-082-430	Sequence 430, App
73	45.5	7	14	US-10-293-371-26	Sequence 26, Appl
74	45.5	7	14	US-10-321-648-10	Sequence 10, Appl
75	45.5	7	15	US-10-367-580-196	Sequence 196, App
76	45.5	7	15	US-10-367-593-196	Sequence 196, App
77	45.5	7	15	US-10-367-594-196	Sequence 196, App
78	45.5	7	15	US-10-367-654-196	Sequence 196, App
79	45.5	7	15	US-10-367-658-196	Sequence 196, App
80	45.5	7	15	US-10-367-668-196	Sequence 196, App
81	45.5	7	16	US-10-367-674-196	Sequence 196, App
82	45.5	7	16	US-10-727-335-38	Sequence 38, Appl
83	45.5	7	17	US-10-759-731A-128	Sequence 128, App
84	45.5	7	17	US-10-939-309-137	Sequence 137, App

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85      20 45.5 7 18 US-10-783-786-48 Sequence 48, Appl
86      20 45.5 7 19 US-11-014-403-1 Sequence 1, Appl
87      19 43.2 4 16 US-10-401-131-1 Sequence 1, Appl
88      19 43.2 5 10 US-09-972-656-34 Sequence 34, Appl
89      19 43.2 5 10 US-09-972-656-36 Sequence 36, Appl
90      19 43.2 5 10 US-09-972-656-40 Sequence 40, Appl
91      19 43.2 5 14 US-10-190-082-240 Sequence 240, App
92      19 43.2 5 14 US-10-247-960-12 Sequence 12, Appl
93      19 43.2 5 15 US-10-338-366-26 Sequence 26, Appl
94      19 43.2 5 15 US-10-436-549-362 Sequence 362, App
95      19 43.2 5 15 US-10-243-613-82 Sequence 82, Appl
96      19 43.2 5 16 US-10-712-425-362 Sequence 362, App
97      19 43.2 5 16 US-10-401-131-2 Sequence 2, Appl
98      19 43.2 5 17 US-10-773-032-362 Sequence 362, App
99      19 43.2 5 17 US-10-923-257-1 Sequence 1, Appl
100     19 43.2 6 10 US-09-809-638-746 Sequence 746, App

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## ALIGNMENTS

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RESULT 1
US-09-782-650-1
; Sequence 1, Application US/09782650
; Patent No. US20020019350A1
; GENERAL INFORMATION:
; APPLICANT: Levine, Arnold J.
; APPLICANT: Mitterer, Artur
; APPLICANT: Falkner, Falko-Guenter
; APPLICANT: Scheiflinger, Friedrich
; APPLICANT: Dörner, Friedrich
; APPLICANT: Edwards Lifesciences Corporation
; TITLE OF INVENTION: Targeted Angiogenesis
; FILE REFERENCE: 20553D-000611US
; CURRENT APPLICATION NUMBER: US/09/782,650
; CURRENT FILING DATE: 2001-02-12
; PRIOR APPLICATION NUMBER: US 09/324,079
; PRIOR FILING DATE: 1999-06-01
; PRIOR APPLICATION NUMBER: US 09/327,045
; PRIOR FILING DATE: 1999-06-07
; PRIOR APPLICATION NUMBER: PCT/US00/14988
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:targeting
; OTHER INFORMATION: molecule
US-09-782-650-1

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Query Match 100.0%; Score 44; DB 9; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGGVFWQ 7
Db 1 GGGVFWQ 7

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RESULT 2
US-09-910-582B-2
; Sequence 2, Application US/09910582B
; Publication No. US20030045476A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Mackenna, Deirdre A.
; TITLE OF INVENTION: Heart Homing Conjugates
; FILE REFERENCE: P-LJ 4857
; CURRENT APPLICATION NUMBER: US/09/910,582B
; CURRENT FILING DATE: 2001-07-20

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; PRIOR APPLICATION NUMBER: US 09/326,718
; PRIOR FILING DATE: 1999-06-07
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-09-910-582B-2

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Query Match 100.0%; Score 44; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGGVFWQ 7
Db 1 GGGVFWQ 7

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RESULT 3
US-10-838-289-34
; Sequence 34, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Heart homing peptide
US-10-838-289-34

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Query Match 100.0%; Score 44; DB 17; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 GGGVFWQ 7
Db 1 GGGVFWQ 7

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RESULT 4
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; Sequence 100, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jinming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756

```

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; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 100
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Ovary homing peptide
US-10-838-289-100

Query Match          61.4%; Score 27; DB 17; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGVFWQ 7
Db 1 GGDVWWR 7

RESULT 5
US-10-607-595-300
; Sequence 300, Application US/10607595
; Publication No. US20050074812A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/10/607,595
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 300
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-300

Query Match          61.4%; Score 27; DB 17; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGVFWQ 7
Db 1 GGDVWWR 7

RESULT 6
US-10-190-082-185
; Sequence 185, Application US/10190082
; Publication No. US20030148264A1
; GENERAL INFORMATION:
; APPLICANT: Laeky, Lawrence A.
; APPLICANT: Sidhu, Sachdev S.
; APPLICANT: Held, Heike A.
; TITLE OF INVENTION: PHAGE DISPLAYED PDZ DOMAIN LIGANDS
; FILE REFERENCE: P1905R1
; CURRENT APPLICATION NUMBER: US/10/190,082
; CURRENT FILING DATE: 2002-07-03
; PRIOR APPLICATION NUMBER: US 60/303,634
; PRIOR FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 683
; SEQ ID NO 185
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
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; OTHER INFORMATION: Synthetic
US-10-190-082-185

Query Match          59.1%; Score 26; DB 14; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 GGGVFW 6
Db 1 GGGCSW 6

RESULT 7
US-09-940-727B-60
; Sequence 60, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 60
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-60

Query Match          56.8%; Score 25; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GGGVF 5
Db 1 GGGLF 5

RESULT 8
US-09-940-727B-63
; Sequence 63, Application US/09940727B
; Publication No. US2003007793A1
; GENERAL INFORMATION:
; APPLICANT: Landry, Donald W
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
; FILE REFERENCE: 0575/51400-B
; CURRENT APPLICATION NUMBER: US/09/940,727B
; CURRENT FILING DATE: 2002-09-04
; PRIOR APPLICATION NUMBER: 09/214,095
; PRIOR FILING DATE: 1998-12-28
; PRIOR APPLICATION NUMBER: PCT/US97/10965
; PRIOR FILING DATE: 1997-06-25
; PRIOR APPLICATION NUMBER: 08/672,345
; PRIOR FILING DATE: 1996-06-25
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 63
; LENGTH: 7
; TYPE: PRT
; ORGANISM: mouse
US-09-940-727B-63

Query Match          56.8%; Score 25; DB 10; Length 7;
Best Local Similarity 80.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
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QY 1 GGVVF 5  
|||:|  
Db 1 GGGLF 5

RESULT 9  
US-09-940-727B-66  
; Sequence 66, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 66  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: mouse  
US-09-940-727B-66

Query Match 56.8%; Score 25; DB 10; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVVF 5  
|||:|  
Db 1 GGGLF 5

RESULT 10  
US-09-940-727B-78  
; Sequence 78, Application US/09940727B  
; Publication No. US2003007793A1  
; GENERAL INFORMATION:  
; APPLICANT: Landry, Donald W  
; TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY  
; FILE REFERENCE: 0575/51400-B  
; CURRENT APPLICATION NUMBER: US/09/940,727B  
; CURRENT FILING DATE: 2002-09-04  
; PRIOR APPLICATION NUMBER: 09/214,095  
; PRIOR FILING DATE: 1998-12-28  
; PRIOR APPLICATION NUMBER: PCT/US97/10965  
; PRIOR FILING DATE: 1997-06-25  
; PRIOR APPLICATION NUMBER: 08/672,345  
; PRIOR FILING DATE: 1996-06-25  
; NUMBER OF SEQ ID NOS: 121  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 78  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: mouse  
; FEATURE:  
; NAME/KEY: MISC FEATURE  
; LOCATION: (7)..(7)  
; OTHER INFORMATION: any amino acid  
US-09-940-727B-78

Query Match 56.8%; Score 25; DB 10; Length 7;  
Best Local Similarity 80.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGVVF 5  
|||:|  
Db 1 GGGLF 5

RESULT 11  
US-10-312-316-3  
; Sequence 3, Application US/10312316  
; Publication No. US2004013751A1  
; GENERAL INFORMATION:  
; APPLICANT: Genentech, Inc.  
; APPLICANT: Devaux, Brigitte  
; APPLICANT: Hongo, Jo-Anne S.  
; APPLICANT: Presta, Leonard G.  
; APPLICANT: Shelton, David L.  
; TITLE OF INVENTION: AGONIST ANTI-TRK-C MONOCLONAL ANTIBODIES  
; FILE REFERENCE: GENENT.0400PC  
; CURRENT APPLICATION NUMBER: US/10/312,316  
; CURRENT FILING DATE: 2002-12-20  
; PRIOR APPLICATION NUMBER: 60/238,319  
; PRIOR FILING DATE: 2000-10-05  
; NUMBER OF SEQ ID NOS: 89  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-312-316-3

Query Match 56.8%; Score 25; DB 16; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
|||:|  
Db 2 GGYW 6

RESULT 12  
US-10-893-576-95  
; Sequence 95, Application US/10893576  
; Publication No. US20050118643A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGESS, TERESA L.  
; APPLICANT: COXON, ANGELA  
; APPLICANT: GREEN, LARRY L.  
; APPLICANT: ZHANG, KE  
; TITLE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR  
; FILE REFERENCE: 06843.0051-00000  
; CURRENT APPLICATION NUMBER: US/10/893,576  
; CURRENT FILING DATE: 2004-07-16  
; PRIOR APPLICATION NUMBER: US 60/488,681  
; PRIOR FILING DATE: 2003-07-18  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 95  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy chain  
; OTHER INFORMATION: variable region CDR peptide  
US-10-893-576-95

Query Match 56.8%; Score 25; DB 17; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
|||:|  
Db 2 GGYW 6

RESULT 13  
US-10-893-576-98  
; Sequence 98, Application US/10893576



Publication No. US20050118643A1  
; GENERAL INFORMATION:  
; APPLICANT: BURGESS, TERESA L.  
; APPLICANT: COXON, ANGELA  
; APPLICANT: GREEN, LARRY L.  
; APPLICANT: ZHANG, KE  
; FILE OF INVENTION: SPECIFIC BINDING AGENTS TO HEPATOCYTE GROWTH FACTOR  
; FILE REFERENCE: 06843.0051-00000  
; CURRENT APPLICATION NUMBER: US/10/893,576  
; CURRENT FILING DATE: 2004-07-16  
; PRIOR APPLICATION NUMBER: US 60/488,681  
; PRIOR FILING DATE: 2003-07-18  
; NUMBER OF SEQ ID NOS: 194  
; SOFTWARE: PatentIn Ver. 3.2  
; SEQ ID NO 98  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic heavy chain  
; OTHER INFORMATION: variable region CDR peptide  
US-10-893-576-98

Query Match 56.8%; Score 25; DB 17; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
|||:  
Db 2 GGYW 6

RESULT 14  
US-10-984-960A-22  
; Sequence 22, Application US/10984960A  
; Publication No. US20050142137A1  
; GENERAL INFORMATION:  
; APPLICANT: Gallo, Michael  
; APPLICANT: Chui, Daniel  
; APPLICANT: Zhong, Haihong  
; APPLICANT: Ara, Gulshan  
; APPLICANT: Larocheille, William J.  
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR  
; FILE REFERENCE: Cura 970  
; CURRENT APPLICATION NUMBER: US/10/984,960A  
; CURRENT FILING DATE: 2004-11-08  
; PRIOR APPLICATION NUMBER: 60/518,275  
; PRIOR FILING DATE: 2003-11-07  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 22  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-984-960A-22

Query Match 56.8%; Score 25; DB 18; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
|||:  
Db 2 GGYW 6

RESULT 15  
US-10-984-960A-77  
; Sequence 77, Application US/10984960A  
; Publication No. US20050142137A1  
; GENERAL INFORMATION:  
; APPLICANT: Gallo, Michael  
; APPLICANT: Chui, Daniel  
; APPLICANT: Zhong, Haihong

APPLICANT: Ara, Gulshan  
; APPLICANT: Larocheille, William J.  
; TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR  
; FILE REFERENCE: Cura 970  
; CURRENT APPLICATION NUMBER: US/10/984,960A  
; CURRENT FILING DATE: 2004-11-08  
; PRIOR APPLICATION NUMBER: 60/518,275  
; PRIOR FILING DATE: 2003-11-07  
; NUMBER OF SEQ ID NOS: 112  
; SOFTWARE: CuraSeqList version 0.1  
; SEQ ID NO 77  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-984-960A-77

Query Match 56.8%; Score 25; DB 18; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 GGVFW 6  
|||:  
Db 2 GGYW 6

Search completed: August 3, 2005, 12:13:59  
Job time : 90.3333 secs

**This Page Blank (uspto)**

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 19 Seconds  
(without alignments)  
35.448 Million cell updates/sec

Title: US-09-910-582B-3

Perfect score: 43

Sequence: 1 HGVVRPH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 457

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR\_79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	39.5	6	2 JN0861	peptidyl-dipeptida
2	16	37.2	7	2 I48105	dihydrofolate redu
3	15	34.9	5	2 JN0860	peptidyl-dipeptida
4	15	34.9	5	2 JN0862	peptidyl-dipeptida
5	14	32.6	3	3 A60898	bursin - chicken
6	14	32.6	5	2 I40702	primase - Citrobac
7	13	30.2	7	2 A15398	choline oxidase (E
8	12	27.9	5	2 S53595	hypothetical prote
9	12	27.9	7	2 S16364	opacity protein P.
10	12	27.9	7	2 S16365	opacity protein P.
11	12	27.9	7	2 E33932	Ig mu chain D regi
12	11	25.6	4	1 ECXAA	antho-RFamide neur
13	11	25.6	4	2 A25844	antho-RF amide neu
14	11	25.6	5	2 PT0553	T-cell receptor be
15	11	25.6	5	2 PT0608	T-cell receptor be
16	11	25.6	6	2 PQ0008	angiotensin-conver
17	11	25.6	6	2 A60494	antineoplastic gly
18	11	25.6	6	2 I51434	H4 histone - Afric
19	11	25.6	6	2 B33922	Ig mu chain D regi
20	11	25.6	7	2 PT0667	T-cell receptor be
21	11	25.6	7	2 PT0655	T-cell receptor be
22	11	25.6	7	2 A58718	carnocin U149 - Ca
23	10	23.3	4	2 S17255	ribosomal protein
24	10	23.3	6	2 A20186	fatty-acid synthas
25	10	23.3	7	2 A28709	phosphonoacetaldeh
26	10	23.3	7	2 S42620	aggrecaen - bovine
27	9	20.9	3	3 PQ0010	angiotensin-conver
28	9	20.9	4	2 A02147	phagocytosis-stimu
29	9	20.9	4	2 T30569	hypothetical prote

30	9	20.9	5	1	HOR0HA	proctolin - Americ
31	9	20.9	5	2	C41225	copper resistance
32	9	20.9	5	2	A60411	proctolin - Atlant
33	9	20.9	6	2	S11024	hydrogensulfite re
34	9	20.9	6	2	A61140	sperm acrosomal pr
35	9	20.9	6	2	I37027	protamine P1 - gor
36	9	20.9	6	2	S78764	ribosomal protein
37	9	20.9	6	2	B26206	alpha-1,4-glucan-p
38	9	20.9	6	2	PT0568	T-cell receptor be
39	9	20.9	7	2	A60224	Met-enkephalin-Arg
40	9	20.9	7	2	A44428	platelet aggregati
41	9	20.9	7	2	A34818	vicilin 72K chain
42	9	20.9	7	2	A33098	244K exoantigen -
43	9	20.9	7	2	PT0520	T-cell receptor be
44	9	20.9	7	2	PT0620	T-cell receptor be
45	9	20.9	7	2	A39690	neural cell adhesi
46	9	20.9	7	2	PQ0777	NADH2 dehydrogenas
47	9	20.9	7	2	A61081	tryptophyllin, bas
48	8	18.6	3	3	RHSHT	thyroliberin - she
49	8	18.6	3	3	A92971	thyroliberin - eas
50	8	18.6	3	3	RHTDIO	thyroliberin - Bom
51	8	18.6	3	3	GKHU	growth-modulating
52	8	18.6	3	3	RHPGT	thyroliberin - pig
53	8	18.6	4	2	A48360	gamma subunit of P
54	8	18.6	4	2	I38888	COI intron 16 prot
55	8	18.6	4	2	S39390	myosin-light-chain
56	8	18.6	4	2	PL0140	carbon-monoxide de
57	8	18.6	4	2	PT0271	Ig heavy chain CRD
58	8	18.6	4	2	PT0712	T-cell receptor be
59	8	18.6	5	2	S70154	URF2 protein - xan
60	8	18.6	5	2	T10954	hypothetical prote
61	8	18.6	5	2	PQ0689	photosystem I 10.4
62	8	18.6	5	2	B61445	Leu-enkephalin - b
63	8	18.6	5	2	A61445	Met-enkephalin - b
64	8	18.6	5	2	S62883	seminal plasma pro
65	8	18.6	5	2	PT0597	T-cell receptor be
66	8	18.6	5	2	PT0572	T-cell receptor be
67	8	18.6	5	2	I40698	biotin B - Citroba
68	8	18.6	5	2	S11075	alcohol dehydrogen
69	8	18.6	6	2	A35890	RNA-directed DNA p
70	8	18.6	6	2	A61419	sarcosine dehydrog
71	8	18.6	6	2	A44916	mosquitocidal toxi
72	8	18.6	6	2	S29637	Jacalin beta-II ch
73	8	18.6	6	2	B56979	collagen alpha 1(I
74	8	18.6	6	2	A46474	Fc epsilon RIIB -
75	8	18.6	6	2	PT0693	T-cell receptor be
76	8	18.6	6	2	S71349	beta-crystallin B2
77	8	18.6	7	1	NYPG7	hypochalamic hepta
78	8	18.6	7	2	A60139	fatty-acid synthas
79	8	18.6	7	2	S21230	dermorphin (Trp-4,
80	8	18.6	7	2	S19630	ribosomal protein -
81	8	18.6	7	2	PQ0663	membrane protein -
82	8	18.6	7	2	S42407	gramicidin S synth
83	8	18.6	7	2	PN0150	omega-gliadin 1,
84	8	18.6	7	2	S71239	ICL2 protein - Par
85	8	18.6	7	2	PC1316	large granule L3 c
86	8	18.6	7	2	I50210	gene c-rel protein
87	8	18.6	7	2	PT0246	Ig heavy chain CRD
88	8	18.6	7	2	PT0283	Ig heavy chain CRD
89	8	18.6	7	2	PT0676	T-cell receptor be
90	8	18.6	7	2	PX0008	glucuronosyltransf
91	8	18.6	7	2	S66442	glutathione S-tran
92	8	18.6	7	2	A38671	peptidylglycine mo
93	8	18.6	7	2	S58797	serine/threonine-s
94	8	18.6	7	2	S29735	polyphosphate-gluc
95	8	18.6	7	2	S09066	globulin IV alpha
96	8	18.6	7	2	I46868	alpha-myosin heavy
97	8	18.6	7	2	S08606	hypothetical prote
98	8	18.6	7	4	I56695	hypothetical L2 pr
99	8	18.6	7	4	S15597	orf 4 rara 5'-regi
100	7	16.3	3	3	A43391	TRH-like tripeptid

## ALIGNMENTS

## RESULT 1

JN0861  
 peptidyl-di-peptidase A inhibitory peptide C111 - striped bonito  
 C;Species: Sarda orientalis (striped bonito)  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C;Accession: JN0861  
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide  
 A;Reference number: JN0859; MUID:94080036; PMID:7764272  
 A;Accession: JN0861  
 A;Molecule type: protein  
 A;Residues: 1-6 <MAT>  
 A;Experimental source: liver  
 C;Comment: The carboxyl end is essential for the protein's expression of angiotensin I-converting enzyme  
 C;Superfamily: bradykinin-potentiating peptide  
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 39.5%; Score 17; DB 2; Length 6;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VRPH 7  
 ||||  
 Db 2 VYPH 5

## RESULT 2

I48105  
 dihydrofolate reductase - Chinese hamster (fragment)  
 C;Species: Cricetus griseus (Chinese hamster)  
 C;Date: 04-Sep-1997 #sequence\_revision 07-Nov-1997 #text\_change 05-Nov-1999  
 C;Accession: I48105  
 R;Azizkhan, J.C.; Vaughn, J.P.; Christy, R.J.; Hamlin, J.L.  
 Biochemistry 25, 6228-6236, 1986  
 A;Title: Nucleotide sequence and nuclease hypersensitivity of the Chinese hamster dihydrofolate reductase  
 A;Reference number: I48105; MUID:97076541; PMID:3024702  
 A;Accession: I48105  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: DNA  
 A;Residues: 1-7 <RES>  
 A;Cross-references: GB:M14771; NID:G191055; PIDN:AAA35975.1; PID:G191056

Query Match 37.2%; Score 16; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VRP 6  
 ||||  
 Db 2 VRP 4

## RESULT 3

JN0860  
 peptidyl-di-peptidase A inhibitory peptide C107 - striped bonito  
 C;Species: Sarda orientalis (striped bonito)  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C;Accession: JN0860  
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide  
 A;Reference number: JN0859; MUID:94080036; PMID:7764272  
 A;Accession: JN0860  
 A;Molecule type: protein  
 A;Residues: 1-5 <MAT>

A;Experimental source: intestine  
 C;Comment: The carboxyl-terminus is essential for the protein's expression of angiotensin I-converting enzyme  
 C;Superfamily: bradykinin-potentiating peptide  
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 34.9%; Score 15; DB 2; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 PH 7  
 ||||  
 Db 3 PH 4

## RESULT 4

JN0862  
 peptidyl-di-peptidase A inhibitory peptide C112 - striped bonito  
 C;Species: Sarda orientalis (striped bonito)  
 C;Date: 10-Mar-1994 #sequence\_revision 10-Mar-1994 #text\_change 07-May-1999  
 C;Accession: JN0862  
 R;Matsumura, N.; Fujii, M.; Takeda, Y.; Shimizu, T.  
 Biosci. Biotechnol. Biochem. 57, 1743-1744, 1993  
 A;Title: Isolation and characterization of angiotensin I-converting enzyme inhibitory peptide  
 A;Reference number: JN0859; MUID:94080036; PMID:7764272  
 A;Accession: JN0862  
 A;Molecule type: protein  
 A;Residues: 1-5 <MAT>

A;Experimental source: intestine  
 C;Comment: The amino terminal tripeptide of this protein inhibits angiotensin I-converting enzyme  
 C;Superfamily: bradykinin-potentiating peptide  
 C;Keywords: angiotensin-converting enzyme inhibitor

Query Match 34.9%; Score 15; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 VRP 6  
 :|||  
 Db 1 IRP 3

## RESULT 5

A60898  
 bursin - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 15-Jun-2001 #sequence\_revision 15-Jun-2001 #text\_change 15-Mar-2004  
 C;Accession: A60898  
 R;Audhya, T.; Kroon, D.; Heavner, G.; Viamontes, G.; Goldstein, G.  
 Science 231, 997-999, 1986  
 A;Title: Tripeptide structure of bursin, a selective B-cell-differentiating hormone of the bursin gene  
 A;Reference number: A60898; MUID:86122916; PMID:3484838  
 A;Accession: A60898  
 A;Molecule type: protein  
 A;Residues: 1-3 <AUD>

C;Keywords: amidated carboxyl end; hormone  
 F;3/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 32.6%; Score 14; DB 3; Length 3;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HG 2  
 ||||  
 Db 2 HG 3

## RESULT 6

I40702  
 primase - Citrobacter diversus (fragment)  
 C;Species: Citrobacter diversus  
 C;Date: 16-Aug-1996 #sequence\_revision 16-Aug-1996 #text\_change 16-Aug-1996  
 C;Accession: I40702  
 R;Versalovic, J.; Lupski, J.R.  
 Mol. Microbiol. 8, 343-355, 1993  
 A;Title: Conservation and evolution of the rpsU-dnaG-rpoD macromolecular synthesis (MMS) genes  
 A;Reference number: I40702; MUID:93302510; PMID:8316085  
 A;Accession: I40702  
 A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA  
 A;Residues: 1-5 <RES>  
 A;Cross-references: GB:L01754; NID:g144439  
 C;Genetics:  
 A;Gene: dnaG

Query Match 32.6%; Score 14; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GRV 4  
 ||:  
 Db 3 GRI 5

RESULT 7  
 A15398  
 choline oxidase (EC 1.1.3.17) - Alcaligenes sp. (tentative sequence) (fragment)  
 C;Species: Alcaligenes sp.  
 C;Date: 05-Jun-1987 #sequence\_revision 05-Jun-1987 #text\_change 09-Jul-2004  
 C;Accession: A15398  
 R;Ohta-Fukuyama, M.; Miyake, Y.; Emi, S.; Yamano, T.  
 J. Biochem. 88, 197-203, 1980

A;Title: Identification and properties of the prosthetic group of choline oxidase from A  
 A;Reference number: A15398; MUID:81006769; PMID:6997283  
 A;Accession: A15398  
 A;Molecule type: protein  
 A;Residues: 1-7 <OHT>  
 A;Cross-references: UNIPROT:P16101  
 C;Keywords: oxidoreductase

Query Match 30.2%; Score 13; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HGR 3  
 ||:  
 Db 5 HSR 7

RESULT 8  
 S53595  
 hypothetical protein (upstream of transcription factor, CCAAT-binding) - chicken  
 C;Species: Gallus gallus (chicken)  
 C;Date: 15-Jul-1995 #sequence\_revision 01-Sep-1995 #text\_change 07-May-1999  
 R;Calkhoven, C.F.; Bouwman, P.R.J.; Snippe, L.; Ab, G.  
 Nucleic Acids Res. 22, 5540-5547, 1994  
 A;Title: Translation start site multiplicity of the CCAAT/enhancer binding protein alpha  
 A;Reference number: S53595; MUID:95140613; PMID:7838705  
 A;Accession: S53595  
 A;Status: preliminary  
 A;Molecule type: DNA  
 A;Residues: 1-5 <CAL>  
 A;Cross-references: EMBL:X66844

Query Match 27.9%; Score 12; DB 2; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GRV 4  
 ||:  
 Db 3 GRL 5

RESULT 9  
 S16364  
 opacity protein P.IIe - Neisseria gonorrhoeae (strain FA1090) (fragment)  
 N;Alternate names: outer membrane protein P.IIe  
 C;Species: Neisseria gonorrhoeae  
 A;Variety: strain FA1090  
 C;Date: 19-Mar-1997 #sequence\_revision 17-Oct-1997 #text\_change 17-Oct-1997  
 C;Accession: S16364

R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.  
 Infect. Immun. 55, 2026-2031, 1987

A;Title: Antigenic and structural differences among six proteins II expressed by a single  
 A;Reference number: S16360; MUID:87306843; PMID:3114142  
 A;Accession: S16364  
 A;Molecule type: protein  
 A;Residues: 1-7 <BAR>

A;Experimental source: strain FA1090

A;Note: expression of opacity proteins is regulated by the number of translated repeat e)  
 of repeats place the start codon in frame with the rest of the protein

C;Superfamily: opacity protein

C;Keywords: cell surface component; transmembrane protein

F;1-7/Product: opacity protein P.IIe (fragment) #status experimental <MAT>

Query Match 27.9%; Score 12; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGR 3  
 ||:  
 Db 5 NGR 7

RESULT 10

S16365

opacity protein P.IIf - Neisseria gonorrhoeae (strain FA1090) (fragment)

N;Alternate names: outer membrane protein P.IIf

C;Species: Neisseria gonorrhoeae

A;Variety: strain FA1090

C;Date: 19-Mar-1997 #sequence\_revision 17-Oct-1997 #text\_change 17-Oct-1997

C;Accession: S16365

R;Barritt, D.S.; Schwalbe, R.S.; Klapper, D.G.; Cannon, J.G.

Infect. Immun. 55, 2026-2031, 1987

A;Title: Antigenic and structural differences among six proteins II expressed by a single

A;Reference number: S16360; MUID:87306843; PMID:3114142

A;Accession: S16365

A;Molecule type: protein

A;Residues: 1-7 <BAR>

A;Experimental source: strain FA1090

A;Note: expression of opacity proteins is regulated by the number of translated repeat e)  
 of repeats place the start codon in frame with the rest of the protein

C;Superfamily: opacity protein

C;Keywords: cell surface component; transmembrane protein

F;1-7/Product: opacity protein P.IIf (fragment) #status experimental <MAT>

Query Match 27.9%; Score 12; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGR 3  
 ||:  
 Db 5 NGR 7

RESULT 11

E33932

Ig mu chain D region (E7) - mouse

C;Species: Mus musculus (house mouse)

C;Date: 09-Mar-1990 #sequence\_revision 09-Mar-1990 #text\_change 16-Aug-1996

C;Accession: E33932

R;Baccala, R.; Vo Quang, T.; Gilbert, M.; Ternynck, T.; Avrameas, S.

Proc. Natl. Acad. Sci. U.S.A. 86, 4624-4628, 1989

A;Title: Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-lin

A;Reference number: A33932; MUID:89282823; PMID:2499887

A;Accession: E33932

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-7 <BAC>

A;Cross-references: GB:M27106

C;Keywords: immunoglobulin

Query Match 27.9%; Score 12; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RP 6  
||

Db 1 RP 2

#### RESULT 12

ECXXA

antho-RFamide neuropeptide - sea anemone (Anthopleura elegantissima)

C;Species: Anthopleura elegantissima

C;Date: 31-Dec-1988 #sequence\_revision 31-Dec-1988 #text\_change 09-Jul-2004

C;Accession: A26666

R;Grimmelikhuijzen, C.J.P.; Graff, D.

Proc. Natl. Acad. Sci. U.S.A. 83, 9817-9821, 1986

A;Title: Isolation of <Glu-Gly-Arg-Phe-NH<sub>2</sub> (Antho-RFamide), a neuropeptide from sea anem

A;Reference number: A26666; MUID: 87092339; PMID: 2879288

A;Accession: A26666

A;Molecule type: protein

A;Residues: 1-4 <GRI>

A;Cross-references: UNIPROT:P10419

C;Comment: The function of this peptide is not known but it could act as a transmitter a

C;Superfamily: RFamide neuropeptide

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 25.6%; Score 11; DB 1; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GR 3  
||

Db 2 GR 3

#### RESULT 13

A25844

autho-RF amide neuropeptide - sea pansy (Renilla koellikeri)

C;Species: Renilla koellikeri (Koelliker's sea pansy)

C;Date: 21-May-1988 #sequence\_revision 30-Sep-1993 #text\_change 11-Jul-1997

C;Accession: A25844

R;Grimmelikhuijzen, C.J.P.; Groeger, A.

FEBS Lett. 211, 105-108, 1987

A;Title: Isolation of the neuropeptide pGlu-Gly-Arg-Phe-amide from the pennatulid Renill

A;Reference number: A25844

A;Accession: A25844

A;Molecule type: protein

A;Residues: 1-4 <GRI>

C;Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

F;4/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 25.6%; Score 11; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GR 3  
||

Db 2 GR 3

#### RESULT 14

PT0553

T-cell receptor beta chain V-D-J region (126-1C) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 30-May-1997

C;Accession: PT0553

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID: 91277601; PMID: 1711558

A;Accession: PT0553

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Experimental source: day 18 fetal thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 25.6%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GR 3  
||

Db 3 GR 4

#### RESULT 15

PT0608

T-cell receptor beta chain V-D-J region (120-2CF) - mouse (fragment)

C;Species: Mus musculus (house mouse)

C;Date: 17-Jul-1992 #sequence\_revision 17-Jul-1992 #text\_change 09-Jul-2004

C;Accession: PT0608

R;Feeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A;Reference number: PT0509; MUID: 91277601; PMID: 1711558

A;Accession: PT0608

A;Status: translation not shown

A;Molecule type: mRNA

A;Residues: 1-5 <FEE>

A;Cross-references: UNIPROT:O18345

A;Experimental source: newborn thymus, strain BALB/c

C;Keywords: T-cell receptor

Query Match 25.6%; Score 11; DB 2; Length 5;

Best Local Similarity 100.0%; Pred. No. 2.8e+05;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 GR 3  
||

Db 3 GR 4

Search completed: August 3, 2005, 11:42:32

Job time : 20 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 88.6667 Seconds  
(without alignments)  
40.427 Million cell updates/sec

Title: US-09-910-582B-3  
Perfect score: 43  
Sequence: 1 HGRVRPH 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_03:\*

1: uniprot\_sprot:.\*  
2: uniprot\_trembl:.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	39.5	6	1	PVFL_PENNO
2	13	30.2	7	1	CHOX_ALCSP
3	12	27.9	7	2	O98866
4	12	27.9	7	2	O98866
5	11	25.6	5	1	E103_LITRU
6	11	25.6	5	1	UF01_MOUSE
7	11	25.6	7	1	LANC_CARUI
8	10	23.3	4	1	YIM1_YEAST
9	10	23.3	7	1	FAF2_ASCSU
10	10	23.3	7	1	FAF2_PANRE
11	10	23.3	7	1	FAF4_PANRE
12	10	23.3	7	2	Q8TAQ4
13	10	23.3	7	2	P82445
14	10	23.3	7	2	Q83480
15	9	20.9	4	1	TUFT_HUMAN
16	9	20.9	5	1	PRCT_CARMA
17	9	20.9	5	1	PRCT_LIMPO
18	9	20.9	5	1	PRCT_PERAM
19	9	20.9	6	1	QVM_LPDDE
20	9	20.9	6	1	VP15_HVHK
21	9	20.9	7	1	ALL3_CARMA
22	9	20.9	7	1	ALL4_CARMA
23	9	20.9	7	1	ALL5_CARMA
24	9	20.9	7	1	GRFP_MOUSE
25	9	20.9	7	1	TPFY_PACDA
26	9	20.9	7	1	UF04_MOUSE
27	9	20.9	7	1	UN06_PINPS
28	9	20.9	7	2	Q8NH77
29	9	20.9	7	2	O07354
30	8	18.6	3	1	GRMM_HUMAN
31	8	18.6	3	1	THYL_BOMOR

32	8	18.6	3	1	THYL_NOTVI
33	8	18.6	3	1	THYL_PIG
34	8	18.6	3	1	THYL_SHEEP
35	8	18.6	4	1	DCML_PSECH
36	8	18.6	4	1	FVRI_ATEL
37	8	18.6	5	1	BIOB_CITFR
38	8	18.6	5	1	E104_LITRU
39	8	18.6	5	1	FARP_ARTTR
40	8	18.6	5	2	Q99007
41	8	18.6	6	1	SAPP_SEPOF
42	8	18.6	6	1	TMOF_SARBU
43	8	18.6	6	1	TRPI_PSEPU
44	8	18.6	7	1	FAFI_ASCSU
45	8	18.6	7	1	FAR5_HIRME
46	8	18.6	7	1	HV7_PIG
47	8	18.6	7	1	TY51_LITRU
48	8	18.6	7	1	UF03_MOUSE
49	8	18.6	7	2	Q28742
50	8	18.6	7	2	Q99182
51	8	18.6	7	2	Q9C5B3
52	8	18.6	7	2	P72081
53	8	18.6	7	2	Q47029
54	8	18.6	7	2	Q8K3H6
55	8	18.6	7	2	Q65578
56	8	18.6	7	2	Q66205
57	8	18.6	7	2	Q67113
58	7	16.3	4	2	Q16047
59	7	16.3	5	1	BPP7_BOTIN
60	7	16.3	5	1	FARP_CHICK
61	7	16.3	5	1	PAP2_PARMA
62	7	16.3	5	1	SUGA_ACHDO
63	7	16.3	6	1	CIP1_MYTED
64	7	16.3	6	1	CIP2_MYTED
65	7	16.3	6	1	E101_LITRU
66	7	16.3	6	2	P82181
67	7	16.3	6	2	P82182
68	7	16.3	7	1	ASCL_ALLAS
69	7	16.3	7	1	BRHP_CONIM
70	7	16.3	7	1	CARP_MYTED
71	7	16.3	7	1	E105_LITRU
72	7	16.3	7	1	FARI_HELTI
73	7	16.3	7	1	FARB_CALVO
74	7	16.3	7	1	ICAO_DACDE
75	7	16.3	7	1	MNPI_LEPDE
76	7	16.3	7	2	P83492
77	7	16.3	7	2	P92210
78	7	16.3	7	2	P92214
79	7	16.3	7	2	P92218
80	7	16.3	7	2	P92221
81	7	16.3	7	2	P92226
82	7	16.3	7	2	P92372
83	7	16.3	7	2	P92381
84	7	16.3	7	2	P92385
85	7	16.3	7	2	P92387
86	7	16.3	7	2	P92390
87	7	16.3	7	2	P92393
88	7	16.3	7	2	P92403
89	7	16.3	7	2	P92421
90	7	16.3	7	2	P92425
91	7	16.3	7	2	P92427
92	7	16.3	7	2	P92430
93	7	16.3	7	2	P92440
94	7	16.3	7	2	P92442
95	7	16.3	7	2	Q8MFY6
96	7	16.3	7	2	O50556
97	7	16.3	7	2	Q66113
98	7	16.3	7	2	Q9Y1Q9
99	7	16.3	7	2	Q9Y1R0
100	7	16.3	7	2	Q9Y1E3

ALIGNMENTS

```

RESULT 1
PYFL_PENMO STANDARD; PRT; 6 AA.
ID AC P84005;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Peptide tyrosine phenylalanine 1 (Pep-PYFL).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE, TISSUE SPECIFICITY, AND MASS SPECTROMETRY.
RC TISSUE=Eyestalk;
RX PubMed=12431727; DOI=10.1016/S0196-9781(02)00176-6;
RA Sithigorngul P., Pupum J., Krungkasem C., Longyant S., Panchan N.,
RA Chaivisuthangkura P., Sithigorngul W., Petsom A.;
RT "Four novel Pf5s: members of NPY/PP peptide superfamily from the
RT eyestalk of the giant tiger prawn Penaeus monodon.";
RL Peptides 23:1895-1906(2002).
CC -1- FUNCTION: May act as a neurotransmitter, neuromodulator or
CC neurohormone.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Limited to neuronal cell bodies, neuronal
CC processes and sinus gland.
CC -1- MASS SPECTROMETRY: MW=801.5; METHOD=MALDI; RANGE=1-6; NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the NPY family.
DR InterPro: IPR001955; Pancreatic hormn.
DR PROSITE; PS00265; PANCREATIC_HORMONE_1; PARTIAL.
DR PROSITE; PS00276; PANCREATIC_HORMONE_2; PARTIAL.
DR Annotation: Direct protein sequencing; Neuropeptide.
KW MOD RES 6 6 Phenylalanine amide (Potential).
FT NON_TER
SQ SEQUENCE 6 AA; 802 MW; 69D41774DCC46000 CRC64;

Query Match 39.5%; Score 17; DB 1; Length 6;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 RVRP 6
DB 1 RARP 4

RESULT 2
CHOX_ALCSP STANDARD; PRT; 7 AA.
ID AC P16101;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Choline oxidase (EC 1.1.3.17) (Fragment).
OS Alcaligenes sp.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Alcaligenes.
OX NCBI_TaxID=512;
RN [1]
RP SEQUENCE.
RX MEDLINE=81006769; PubMed=6997283;
RA Ohta-Fukuyama M., Miyake Y., Emi S., Yamano T.;
RT "Identification and properties of the prosthetic group of choline
RT oxidase from Alcaligenes sp.";
RL J. Biochem. 88:197-203(1980).
CC -1- CATALYTIC ACTIVITY: Choline + O(2) = betaine aldehyde + H(2)O(2).
DR PIR; A15398; A15398
KW Direct protein sequencing; Oxidoreductase.
FT NON_TER
SQ SEQUENCE 7 AA; 839 MW; 7415B1E457644AC0 CRC64;

Query Match 30.2%; Score 13; DB 1; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 HGR 3
DB 5 HSR 7

RESULT 3
O98866 PRELIMINARY; PRT; 7 AA.
ID AC O98866;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome b/f subunit IV (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86120353; PubMed=3003688;
RA Sijben-Mueller G., Hallick R.B., Alt J., Westhoff P., Herrmann R.G.;
RT "Spinach plastid genes coding for initiation factor IF-1, ribosomal
RT protein S11 and RNA polymerase alpha-subunit.";
RL Nucleic Acids Res. 14:1029-1044(1986).
DR EMBL; X03496; CAA27215.1; -.
DR GO; GO:0009507; C:chloroplast; IEA.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 7 AA; 907 MW; 644729D77409C420 CRC64;

Query Match 27.9%; Score 12; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RP 6
DB 3 RP 4

RESULT 4
P93233 PRELIMINARY; PRT; 7 AA.
ID AC P93233;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE 1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14)
DE (Fragment).
GN Name=LE-ACS1B;
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97351561; PubMed=9207843; DOI=10.1023/A:1005800511372;
RA Ostler J.H., Olson D.C., Shiu O.Y., Yang S.F.;
RT "Differential induction of seven 1-aminocyclopropane-1-carboxylate
RT synthase genes by elicitor in suspension cultures of tomato
RT (Lycopersicon esculentum).";
RL Plant Mol. Biol. 34:275-286(1997).
DR EMBL; U75692; AAC49682.1; -.
DR GO; GO:0016847; F:1-aminocyclopropane-1-carboxylate synthase . . .; IEA.
DR GO; GO:0016829; F:lyase activity; IEA.
KW Lyase.
FT NON_TER
SQ SEQUENCE 7 AA; 828 MW; 71B412C7377415D0 CRC64;

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Query Match 27.9%; Score 12; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RP 6  
||  
DB 2 RP 3

RESULT 5  
ID E103 LITRU STANDARD; PRT; 5 AA.  
AC P20209;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Electrin 3.  
OS Litoria rubella (Desert tree frog).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
OC Pelodyadinae; Litoria.  
OX NCBI\_TaxID=104895;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Skin secretion;  
RA Wabnitz P.A., Bowie J.H., Tyler M.J., Wallace J.C.;  
RT "Peptides from the skin glands of the Australian buzzing tree frog  
RT Litoria electrica. Comparison with the skin peptides from Litoria  
RT rubella".  
RL Aust. J. Chem. 52:639-645 (1999).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- TISSUE SPECIFICITY: Skin.  
KW Amidation; Amphibian defense peptide; Direct protein sequencing.  
FT MOD RES 5  
SQ SEQUENCE 5 AA; 630 MW; 668761F2C9A00000 CRC64;

Query Match 25.6%; Score 11; DB 1; Length 5;  
Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VRP 6  
||  
DB 2 VHP 4

RESULT 6  
ID UF01 MOUSE STANDARD; PRT; 5 AA.  
AC P38639;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 01-OCT-1994 (Rel. 30, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Unknown protein from 2D-PAGE of fibroblasts (P19) (Fragment).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE.  
RC TISSUE=Fibroblast;  
RX MEDLINE=9500907; PubMed=7523108;  
RA Merrick B.A., Patterson R.M., Wichter L.L., He C., Selkirk J.K.;  
RT "Separation and sequencing of familial and novel murine proteins using  
RT preparative two-dimensional gel electrophoresis".  
RL Electrophoresis 15:735-745 (1994).  
CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown  
CC protein is: 6.6, its MW is: 19 kDa.  
KW Direct protein sequencing.  
FT NON TER 5  
SQ SEQUENCE 5 AA; 717 MW; 7364087043100000 CRC64;

Query Match 25.6%; Score 11; DB 1; Length 5;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 2 GR 3  
||  
DB 3 GR 4

RESULT 7  
ID LANC CARUI STANDARD; PRT; 7 AA.  
AC P36950;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Lantibiotic carnocin UI49 (Fragment).  
OS Carnobacterium sp. (strain UI49).  
OC Bacteria; Firmicutes; Lactobacillales; Carnobacteriaceae;  
OC Carnobacterium  
OX NCBI\_TaxID=35782;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=92321768; PubMed=1622206;  
RA Stoffels G., Nissen-Meyer J., Gudmundsdottir A., Sletten K., Holo H.,  
RA Nes I.F.;  
RT "Purification and characterization of a new bacteriocin isolated from  
RT a Carnobacterium sp.";  
RL Appl. Environ. Microbiol. 58:1417-1422 (1992).  
CC -1- FUNCTION: Lanticholine-containing peptide antibiotic (lantibiotic).  
CC Active on Gram-positive bacteria.  
KW Antibiotic; Bacteriocin; Direct protein sequencing; Lantibiotic.  
FT NON TER 7  
SQ SEQUENCE 7 AA; 786 MW; 741776D05B05B810 CRC64;

Query Match 25.6%; Score 11; DB 1; Length 7;  
Best Local Similarity 33.3%; Pred. No. 1.6e+06;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 VRP 6  
||  
DB 4 IQP 6

RESULT 8  
ID YLM1 YEAST STANDARD; PRT; 4 AA.  
AC P36515;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 01-JUN-1994 (Rel. 29, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).  
GN Names=Yml1;  
OS Saccharomyces cerevisiae (Baker's yeast).  
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;  
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.  
OX NCBI\_TaxID=4932;  
RN [1]  
RP SEQUENCE.  
RX MEDLINE=91285106; PubMed=2060626; DOI=10.1016/0014-5793(91)80759-V;  
RA Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.,  
RA Kitakawa M.;  
RT "Extended N-terminal sequencing of proteins of the large ribosomal  
RT subunit from yeast mitochondria".  
RL FEBS Lett. 284:51-56 (1991).  
CC -1- FUNCTION: Putative component of the large subunit of mitochondrial  
CC ribosome.  
CC -1- SUBCELLULAR LOCATION: Mitochondrial.  
DR PIR; S17255; S17255.  
KW Direct protein sequencing; Mitochondrion; Ribosomal protein.  
FT NON TER 4  
SQ SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;

Query Match 23.3%; Score 10; DB 1; Length 4;  
Best Local Similarity 66.7%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 VRP 6

Db 2 VTP 4

# RESULT 9

FAF2\_ASCSU STANDARD; PRT; 7 AA.  
 AC P67879; P31890;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE FMRFamide-like neuropeptide AF2.  
 OS Ascaris suum (pig roundworm) (Ascaris lumbricoides).  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;  
 OC Ascarididae; Ascaris.  
 OX NCBI\_TaxID=6253;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=93324431; PubMed=8332542; DOI=10.1016/0196-9781(93)90127-3;  
 RA Cowden C., Stretton A.O.W.;  
 RT "AF2, an Ascaris neuropeptide: Isolation, sequence, and bioactivity."  
 RL Peptides 14:423-430(1993).  
 CC -1- FUNCTION: Has effects on muscle tension.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.  
 CC Amidation; Direct protein sequencing; Neuropeptide.  
 KW MOD\_RES 7 Phenylalanine amide.  
 FT MOD\_RES 7 Phenylalanine amide.  
 SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match 23.3%; Score 10; DB 1; Length 7;

Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGRVR 5

Db 2 HEYLR 6

# RESULT 10

FAF2\_PANRE STANDARD; PRT; 7 AA.  
 AC P67880; P31890;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE FMRFamide-like neuropeptide AF2.  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=95060998; PubMed=7970891;  
 RA Maule A.G., Shaw C., Bowman J.W.;  
 RT "The FMRFamide-like neuropeptide AF2 (Ascaris suum) is present in the free-living nematode, Panagrellus redivivus (Nematoda, Rhabditida)."  
 RL Parasitology 109:351-356(1994).  
 CC -1- FUNCTION: Has effects on muscle tension.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Found in the nerve cords and a variety of ganglia particularly in the anterior regions.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.  
 CC Amidation; Direct protein sequencing; Neuropeptide.  
 KW MOD\_RES 7 Phenylalanine amide.  
 FT MOD\_RES 7 Phenylalanine amide.  
 SQ SEQUENCE 7 AA; 992 MW; 69D4073B5B11E350 CRC64;

Query Match 23.3%; Score 10; DB 1; Length 7;  
 Best Local Similarity 40.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGRVR 5

Db 2 HEYLR 6

Query Match 23.3%; Score 10; DB 1; Length 7;

Best Local Similarity 40.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGRVR 5

Db 2 HEYLR 6

# RESULT 11

FAF4\_PANRE STANDARD; PRT; 7 AA.  
 AC P41875;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE FMRFamide-like neuropeptide PF4 (KPNFIRF-amide).  
 OS Panagrellus redivivus.  
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida;  
 OC Panagrolaimoidea; Panagrolaimidae; Panagrellus.  
 OX NCBI\_TaxID=6233;  
 RN [1]  
 RP SEQUENCE, AND SYNTHESIS.  
 RX MEDLINE=95232026; PubMed=7716079; DOI=10.1016/0196-9781(94)00162-Y;  
 RA Maule A.G., Shaw C., Bowman J.W., Halton D.W., Thompson D.P., Thim L., Kubiak T.M., Martin R.A., Geary T.G.;  
 RT "Isolation and preliminary biological characterization of KPNFIRFamide, a novel FMRFamide-related peptide from the free-living nematode, Panagrellus redivivus."  
 RL Peptides 16:87-93(1995).  
 CC -1- FUNCTION: Myoactive; induces a rapid concentration-dependent muscle tension increase.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the FARP (FMRFamide related peptide) family.  
 CC Amidation; Direct protein sequencing; Neuropeptide.  
 KW MOD\_RES 7 Phenylalanine amide.  
 FT MOD\_RES 7 Phenylalanine amide.  
 SQ SEQUENCE 7 AA; 921 MW; 69D40059C4576350 CRC64;

Query Match 23.3%; Score 10; DB 1; Length 7;

Best Local Similarity 33.3%; Pred. No. 1.6e+06;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPH 7

Db 1 KPN 3

# RESULT 12

Q8TAQ4 PRELIMINARY; PRT; 7 AA.  
 AC Q8TAQ4;  
 DT 01-JUN-2002 (TrEMBLrel. 21, Created)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)  
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)  
 DE YAP1 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Uterus;  
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettner M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Greenwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.B., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RL and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [2];  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Uterus;  
 RA Strausberg R.;  
 RL Submitted (APR-2002) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: BC026212; AAH26212.2; -;  
 SQ SEQUENCE 7 AA; 848 MW; 6AB2D1B6C2D406F0 CRC64;

Query Match 23.3%; Score 10; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RVR 5  
 Db 2 RVQ 4

RESULT 13  
 P82445 PRELIMINARY; PRT; 7 AA.  
 AC P82445;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 10 kDa cell wall protein (fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamids; Solanales; Solanaceae; Nicotiana.  
 ON NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=cv. PETIT HAVANA;  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture";  
 RL Planta 0:0-0(2000).  
 CC -!- SUBCELLULAR LOCATION: CELL WALL.  
 CC -!- TISSUE SPECIFICITY: XYLEM.  
 DR GO: GO:0005618; C:cell wall; IEA.  
 KW Cell wall.  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;

Query Match 23.3%; Score 10; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 GRV 4  
 Db 4 GHV 6

RESULT 14  
 Q63480 PRELIMINARY; PRT; 7 AA.  
 AC Q63480;  
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)  
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE TR4-NS orphan receptor (fragment).

CN Name=TR4;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96198747; PubMed=8612486; DOI=10.1210/en.137.5.1562;  
 RA Yoshikawa T., Makino S., Gao X.M., King G.Q., Chuang D.M.,  
 RA Detera-Wadleigh S.D.;  
 RT "Splice variants of rat TR4 orphan receptor: differential expression  
 RT of novel sequences in the 5'-untranslated region and C-terminal  
 RT domain";  
 RL Endocrinology 137:1562-1571(1996).  
 DR EMBL: U59125; AAB02827.1; -;  
 DR GO: GO:0004872; F:receptor activity; IEA.  
 KW Receptor.  
 FT NON TER 1  
 SQ SEQUENCE 7 AA; 758 MW; 672AA87864005350 CRC64;

Query Match 23.3%; Score 10; DB 2; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RVR 5  
 Db 1 KIR 3

RESULT 15  
 ID TUFT HUMAN STANDARD; PRT; 4 AA.  
 AC P01858;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Phagocytosis-stimulating peptide (tuftsin).  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 ON NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RC MEDLINE=72187087; PubMed=4112769;  
 RA Nishio K., Constantopoulos A., Satoh P.S., Najjar V.A.;  
 RT "The characteristics, isolation and synthesis of the phagocytosis  
 RT stimulating peptide tuftsin";  
 RL Biochem. Biophys. Res. Commun. 47:172-179(1972).  
 RN [2]  
 RP IMMUNOGLOBULIN CLASS.  
 RX MEDLINE=68091045; PubMed=4169272;  
 RA Fidalgo B.V., Najjar V.A.;  
 RT "The physiological role of the lymphoid system. VI. The stimulatory  
 RT effect of leucophilic gamma globulin (leucokinin) on the phagocytic  
 RT activity of human polymorphonuclear leucocyte.";  
 RL Biochemistry 6:3386-3392(1967).  
 CC -!- MISCELLANEOUS: An IGG (called leucokinin) binds reversibly to the  
 CC cell membrane of neutrophils in the blood. Leucokininase on the  
 CC membrane releases the active peptide tuftsin from the gamma chain.  
 CC Tuftsin is essential for maximum stimulation of the phagocytic  
 CC activity of neutrophils.  
 DR PIR: A02147; A02147.  
 DR MIM: 191150; -;  
 DR GO: GO:0003823; F:antigen binding; NAS.  
 DR GO: GO:0006909; P:phagocytosis; NAS.  
 KW Direct protein sequencing.  
 SQ SEQUENCE 4 AA; 501 MW; 74176321C0000000 CRC64;

Query Match 20.9%; Score 9; DB 1; Length 4;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 1; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RP 6

Db           :|  
              2 KP 3

Search completed: August 3, 2005, 12:07:39  
Job time : 90.6667 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 96.3333 Seconds  
(without alignments)  
28.104 Million cell updates/sec

Title: US-09-910-582B-3

Perfect score: 43

Sequence: 1 HGRVRPH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 121728

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_16Dec04:\*

1: Geneseqp1980s:\*

2: Geneseqp1990s:\*

3: Geneseqp2000s:\*

4: Geneseqp2001s:\*

5: Geneseqp2002s:\*

6: Geneseqp2003as:\*

7: Geneseqp2003bs:\*

8: Geneseqp2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	7	4	AAB30896
2	43	100.0	7	4	AAB50798
3	31	72.1	6	5	ABB77932
4	25	58.1	5	5	ABB77933
5	25	58.1	7	5	ABB77919
6	25	58.1	7	5	ABB77942
7	25	58.1	7	5	ABB77935
8	25	58.1	7	5	ABB77926
9	24	55.8	6	2	AAR83529
10	24	55.8	6	2	AAR84427
11	24	55.8	6	3	AAB14509
12	24	55.8	7	2	ABP98596
13	23	53.5	7	2	AAB74241
14	22	51.2	6	2	AAB87203
15	22	51.2	6	2	AAB74242
16	21	48.8	5	1	AAP90677
17	21	48.8	5	2	AAY34298
18	21	48.8	6	2	AAR20413
19	21	48.8	7	5	ADC35979
20	20.5	47.7	7	5	ABG60380
21	20.5	47.7	7	6	ABR58826
22	20.5	47.7	7	8	ADL95934
23	20	46.5	4	2	AAY13762
24	20	46.5	4	3	AAB14508
25	20	46.5	4	7	AAO29626

26	46.5	4	7	ADD52664
27	46.5	4	8	ADK42403
28	46.5	4	8	ADK42404
29	46.5	5	2	AAR13624
30	46.5	5	7	ADD40737
31	46.5	6	2	AAR87734
32	46.5	6	2	AAW87216
33	46.5	6	3	AAW96490
34	46.5	6	7	ADE10917
35	46.5	6	8	ADRI12844
36	46.5	7	2	AAR59473
37	46.5	7	2	AAR59474
38	46.5	7	2	AAR91327
39	46.5	7	2	AAW45414
40	46.5	7	2	AAW60368
41	46.5	7	2	AAY13795
42	46.5	7	2	AAW93694
43	46.5	7	2	AAY33954
44	46.5	7	2	AAY33955
45	46.5	7	2	AAY33960
46	46.5	7	2	AAY33961
47	46.5	7	3	AAB21785
48	46.5	7	4	AAE06363
49	46.5	7	4	ABP22401
50	46.5	7	5	ABG60853
51	46.5	7	6	AAE31606
52	46.5	7	6	ABR57411
53	46.5	7	6	ABR83390
54	44.2	4	7	ABU10392
55	44.2	4	7	ADF55605
56	44.2	5	2	AAY23538
57	44.2	5	7	ADC13888
58	44.2	5	7	ADC13890
59	44.2	5	8	ADM09850
60	44.2	5	8	ADR71016
61	44.2	6	2	AAW20464
62	44.2	6	2	AAW87134
63	44.2	6	2	AAW87136
64	44.2	6	2	AAW87133
65	44.2	6	2	AAW87135
66	44.2	6	2	AAW87131
67	44.2	6	2	AAW87132
68	44.2	6	2	AAW21747
69	44.2	6	2	AAW05081
70	44.2	6	3	AAB39914
71	44.2	6	4	AAB87889
72	44.2	6	4	AAG71004
73	44.2	6	4	AAE08962
74	44.2	6	4	AAE55481
75	44.2	6	5	ABJ01251
76	44.2	6	6	AAE32833
77	44.2	6	7	ABO32396
78	44.2	6	7	ADE70909
79	44.2	6	7	ADL94402
80	44.2	6	8	ADK72016
81	44.2	6	8	ADO37518
82	44.2	6	8	ADO28040
83	44.2	6	8	ADR50217
84	44.2	7	2	AAR09408
85	44.2	7	2	AAW65198
86	44.2	7	2	AAW10759
87	44.2	7	2	AAW21064
88	44.2	7	2	AAW23187
89	44.2	7	2	AAW30417
90	44.2	7	2	AAW30387
91	44.2	7	2	AAW30443
92	44.2	7	2	AAW20236
93	44.2	7	3	AAW84970
94	44.2	7	3	AAW84984
95	44.2	7	3	AAW67190
96	44.2	7	3	AAW23221
97	44.2	7	3	AAW95630
98	44.2	7	7	ADC44279

Add52664	Angiogene
Adk42403	Antibacte
Adk42404	Antibacte
Aar13624	Peptide f
Add40737	Angiogene
Aar87734	Spacer #3
Aaw87216	Peptide d
Aay96490	Factor VI
Adel0917	Chimeric
Adri12844	HBV surfa
Aar59473	Dynorphin
Aar59474	Dynorphin
Aar91327	Dynorphin
Aaw45414	Hyaluroni
Aaw60368	Tumour ho
Aay13795	Human fac
Aaw93694	Human bre
Aay33954	Dynorphin
Aay33955	Dynorphin
Aay33960	Dynorphin
Aay33961	Dynorphin
Aab21785	Human bre
Aae06363	Human bre
Abp22401	HIV All m
Abg60853	Cellular
Aae31606	Soybean E
Abri57411	Brassica
Abri83390	Human int
Abul0392	Adeonarc
Adf55605	Peptide c
Aay23538	T-cell re
Adc13888	Rheumatoi
Adc13890	Rheumatoi
Adm09850	Human pro
Adr71016	Human pro
Aay20464	Human mic
Aaw87134	Peptide d
Aaw87136	Peptide d
Aaw87133	Peptide d
Aaw87135	Peptide d
Aaw87131	Peptide d
Aaw87132	Peptide d
Aay21747	Conserved
Aay05081	HIV Tat p
Aab39914	Anti-HIV1
Aab87889	Detector
Aag71004	Melanocor
Aae08962	Mammalian
Aab55481	Human ela
Abj01251	Human cas
Aae32833	Human cea
Abo32396	HIV-1 mul
Adc70909	HIV-1 Tat
Adl94402	HIV-1 Tat
Adk72016	Antimicro
Ado37518	Binding p
Ado28040	Capture s
Adr50217	6-mer pep
Aar09408	LFA-1 alp
Aaw65198	Angiotens
Aaw10759	Ferritin
Aaw21064	Lipolytic
Aaw23187	Terminal
Aaw30417	HRE-I aff
Aaw30387	HRE-I aff
Aaw30443	HRE-I aff
Aay20236	Human mic
Aay84970	Amino aci
Aay84984	Amino aci
Aay67190	Cycokine
Aab23221	Hsp47-bin
Aay95630	Peptide u
Adc44279	Endotheli

99 19 44.2 7 7 ADC27877 Synthetic  
100 19 44.2 7 7 AAO23601 Colon tum

## ALIGNMENTS

RESULT 1  
AAB30896  
ID AAB30896 standard; peptide; 7 AA.  
XX AC AAB30896;  
XX DT 02-APR-2001 (first entry)  
XX DE Peptide which selectively binds to normal cardiac endothelium.  
XX KW Cardiac endothelium; angiogenic factor; vascular endothelium;  
XX KW peripheral vascular disease; cardiovascular disease; angiogenesis;  
XX KW cardiac neovascularisation.  
XX OS Unidentified.  
XX PN WO200075329-A1.  
XX PD 14-DEC-2000.  
XX PF 31-MAY-2000; 2000WO-US014988.  
XX PR 07-JUN-1999; 99US-00327045.  
XX PA (EDWA-) EDWARDS LIFESCIENCES CORP.  
XX PA (BAXT) BAXTER AG.  
XX PI Levine AJ, Mitterer A, Falkner F, Scheiflinger F, Dörner F;  
XX DR WPI; 2001-091212/10.  
XX PT New chimeric molecules having an angiogenic factor linked to a targeting  
PT molecule that binds to a vascular endothelium, useful for increasing  
PT cardiac neovascularization, or treating peripheral vascular and  
PT cardiovascular diseases.  
XX PS Disclosure; Page 27; 67pp; English.

XX CC AAB30895-99 represent targeting molecules, which are used to produce the  
CC chimeric molecules of the invention. AAB30895-98 selectively bind to  
CC normal cardiac endothelium. The specification describes a chimeric  
CC molecule comprising an angiogenic factor linked to a targeting molecule  
CC that specifically binds to a vascular endothelium. The chimeric molecules  
CC are useful for treatment of peripheral vascular or cardiovascular  
CC diseases. Specifically, they are useful for inducing or inhibiting  
CC angiogenesis, for increasing cardiac neovascularisation in ischemic  
CC tissue in the peripheral vascular system  
XX SQ Sequence 7 AA;

Query Match 100.0%; Score 43; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7  
DB 1 HGRVRPH 7

RESULT 2  
AAB50798  
ID AAB50798 standard; peptide; 7 AA.  
XX AC AAB50798;  
XX DT 21-MAR-2001 (first entry)

XX DE Heart homing peptide SEQ ID NO: 3.  
XX KW Heart homing peptide; cardiovascular disease; ischaemic disease;  
XX KW gene therapy.  
XX OS Synthetic.  
XX PN WO200075174-A1.  
XX PD 14-DEC-2000.  
XX PF 31-MAY-2000; 2000WO-US015088.  
XX PR 07-JUN-1999; 99US-00326718.  
XX PA (BURN-) BURNHAM INST.  
XX PI Ruoslahti E, Mackenna DA;  
XX DR WPI; 2001-071059/08.  
XX PT Novel heart homing peptide that selectively homes to normal ischemic and  
PT cardiac tissue useful for targeting ischemic tissues for treating  
PT ischemic and cardiovascular diseases such as atherosclerosis and  
PT restenosis.  
XX PS Claim 2; Page 55; 70pp; English.

XX CC The present invention provides a number of heart homing peptides which  
CC selectively home to cardiac tissue. These can be used in the treatment of  
CC cardiovascular and ischaemic diseases, such as atherosclerosis, myocardial  
CC thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial  
CC hypertrophy, congenital heart diseases, ischaemic heart disease and  
CC anginas, acquired valvular/endocardial diseases, primary myocardial  
CC diseases, cardiac tumours and arrhythmias  
XX SQ Sequence 7 AA;

Query Match 100.0%; Score 43; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. NO. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7  
DB 1 HGRVRPH 7

RESULT 3  
AAB77932  
ID ABB77932 standard; peptide; 6 AA.  
XX AC ABB77932;  
XX DT 22-OCT-2002 (first entry)

XX DE Amino acid sequence of cyclopeptide P24 based on VEGF.  
XX KW Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;  
XX KW angiogenesis; tumour growth; metastasis development; ischaemia;  
XX KW vascular eye disease; chronic inflammatory disease; tissue regeneration.  
XX OS Synthetic.

XX PN FR2814744-A1.  
XX PD 05-APR-2002.

XX PF 04-OCT-2000; 2000FR-00012654.  
XX PR 04-OCT-2000; 2000FR-00012654.  
XX PA (COMS) COMMISSARIAT ENERGIE ATOMIQUE.

PA (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.  
 XX (UYBO-) UNIV BORDEAUX 1.  
 PI Betz N, Bikfalvi A, Deleris G;  
 XX WPI; 2002-502486/54.  
 DR  
 XX  
 XX New cyclopeptides containing heptapeptide moiety acting as ligand for the  
 PT KDR receptor of vascular endothelial growth factor (VEGF), useful,  
 PT optionally in supported form, as angiogenesis inhibitors or activators.  
 XX  
 XX Disclosure; Page 45; 66pp; French.  
 PS Claim 3; Page 45; 66pp; French.  
 XX  
 XX The present sequence represents a cyclopeptide, which contains a peptide  
 CC (ABB77919) which is based on a partial sequence of vascular endothelial  
 CC growth factor (VEGF). The arginine and glycine residues of ABB77919 are  
 CC preferably linked by a chain of one or more compounds selected from  
 CC natural or synthetic amino acids and organic compounds selected from  
 CC group and an optionally substituted amino group. The cyclopeptides of the  
 CC invention have high affinity for the KDR receptor of VEGF. The  
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of  
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of  
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of  
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of  
 CC angiogenesis is potentially useful in combating tumour growth, metastasis  
 CC development, ischaemia, vascular eye diseases and chronic inflammatory  
 CC diseases; and promotion of angiogenesis is potentially useful in  
 CC promoting tissue regeneration and colonization of implanted biomaterials  
 CC such as bone substitutes  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 72.1%; Score 31; DB 5; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 GRVRPH 7  
 DB |||:|  
 1 GRKPH 6  
 RESULT 4  
 ABB77913  
 ID ABB77933 standard; peptide; 5 AA.  
 XX  
 AC ABB77933;  
 XX  
 DT 22-OCT-2002 (first entry)  
 XX  
 DE Amino acid sequence of VEGF-based peptide P1.  
 XX  
 KW Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;  
 KW angiogenesis; tumour growth; metastasis development; ischaemia;  
 KW vascular eye disease; chronic inflammatory disease; tissue regeneration.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Modified-site 1  
 FT /note= "H attached"  
 FT Modified-site 5  
 FT /note= "OH attached"  
 FT  
 XX FR2814744-A1.  
 XX  
 XX 05-APR-2002.  
 XX  
 XX 04-OCT-2000; 2000FR-00012654.  
 XX  
 XX 04-OCT-2000; 2000FR-00012654.  
 XX  
 XX (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
 PA (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.  
 PA (UYBO-) UNIV BORDEAUX 1.  
 XX

PI Betz N, Bikfalvi A, Deleris G;  
 XX WPI; 2002-502486/54.  
 DR  
 XX New cyclopeptides containing heptapeptide moiety acting as ligand for the  
 PT KDR receptor of vascular endothelial growth factor (VEGF), useful,  
 PT optionally in supported form, as angiogenesis inhibitors or activators.  
 XX  
 XX Disclosure; Page 42; 66pp; French.  
 PS  
 XX  
 CC The specification describes cyclopeptides, which contain a peptide  
 CC (ABB77919) which is based on a partial sequence of vascular endothelial  
 CC growth factor (VEGF). The arginine and glycine residues of ABB77919 are  
 CC preferably linked by a chain of one or more compounds selected from  
 CC natural or synthetic amino acids and organic compounds have a carboxy  
 CC group and an optionally substituted amino group. The cyclopeptides of the  
 CC invention have high affinity for the KDR receptor of VEGF. The  
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of  
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of  
 CC angiogenesis is potentially useful in combating tumour growth, metastasis  
 CC development, ischaemia, vascular eye diseases and chronic inflammatory  
 CC diseases; and promotion of angiogenesis is potentially useful in  
 CC promoting tissue regeneration and colonization of implanted biomaterials  
 CC such as bone substitutes. The present sequence represents a peptide,  
 CC which is also base don VEGF  
 XX  
 XX Sequence 5 AA;  
 SQ  
 Query Match 58.1%; Score 25; DB 5; Length 5;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 RVRPH 7  
 DB |||:|  
 1 RIKPH 5  
 RESULT 5  
 ABB77919  
 ID ABB77919 standard; peptide; 7 AA.  
 XX  
 AC ABB77919;  
 XX  
 DT 22-OCT-2002 (first entry)  
 XX  
 DE Amino acid sequence of a cyclopeptide based on VEGF.  
 XX  
 KW Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;  
 KW angiogenesis; tumour growth; metastasis development; ischaemia;  
 KW vascular eye disease; chronic inflammatory disease; tissue regeneration.  
 XX  
 OS Synthetic.  
 XX  
 PN FR2814744-A1.  
 XX  
 XX 05-APR-2002.  
 XX  
 XX 04-OCT-2000; 2000FR-00012654.  
 XX  
 XX 04-OCT-2000; 2000FR-00012654.  
 XX  
 XX (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.  
 PA (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.  
 PA (UYBO-) UNIV BORDEAUX 1.  
 XX  
 XX Betz N, Bikfalvi A, Deleris G;  
 XX WPI; 2002-502486/54.  
 DR  
 XX New cyclopeptides containing heptapeptide moiety acting as ligand for the  
 PT KDR receptor of vascular endothelial growth factor (VEGF), useful,  
 PT optionally in supported form, as angiogenesis inhibitors or activators.  
 XX

PS Claim 1; Page 44; 66pp; French.

CC The present sequence represents a cyclopeptide, which is based on a partial sequence of vascular endothelial growth factor (VEGF). The arginine and glycine residues of the present peptide are preferably linked by a chain of one or more compounds selected from natural or synthetic aminoacids and organic compounds have a carboxy group and an optionally substituted amino group. The cyclopeptides of the invention have high affinity for the KDR receptor of VEGF. The cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of angiogenesis is potentially useful in combating tumour growth, metastasis development, ischaemia, vascular eye diseases and chronic inflammatory disease; and promotion of angiogenesis is potentially useful in promoting tissue regeneration and colonization of implanted biomaterials such as bone substitutes

XX  
XX  
SQ Sequence 7 AA;

Query Match 58.1%; Score 25; DB 5; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.8e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7  
|::||  
Db 1 RIKPH 5

RESULT 6

ABB77942

ID ABB77942 standard; peptide; 7 AA.

XX  
AC ABB77942;

XX  
DT 22-OCT-2002 (first entry)

XX  
DE Amino acid sequence of VEGF-based peptide P18.

XX  
KW Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor; angiogenesis; tumour growth; metastasis development; ischaemia; vascular eye disease; chronic inflammatory disease; tissue regeneration.

XX  
OS Synthetic.

FH Key Location/Qualifiers

FT Misc-difference 1 /note= "D-form residue"

FT  
XX  
PN FR2814744-A1.

XX  
PD 05-APR-2002.

XX  
PF 04-OCT-2000; 2000FR-00012654.

XX  
PR 04-OCT-2000; 2000FR-00012654.

XX  
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.

PA (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.

PA (UYBO-) UNIV BORDEAUX 1.

XX  
PI Betz N, Bikfalvi A, Deleris G;

XX  
DR WPI; 2002-502486/54.

XX  
PT New cyclopeptides containing heptapeptide moiety acting as ligand for the KDR receptor of vascular endothelial growth factor (VEGF), useful, optionally in supported form, as angiogenesis inhibitors or activators.

XX  
PS Disclosure; Page 42; 66pp; French.

XX  
CC The specification describes cyclopeptides, which contain a peptide growth factor (VEGF) which is based on a partial sequence of vascular endothelial growth factor (VEGF). The arginine and glycine residues of ABB77919 are preferably linked by a chain of one or more compounds selected from natural or synthetic amino acids and organic compounds have a carboxy

CC preferably linked by a chain of one or more compounds selected from natural or synthetic amino acids and organic compounds have a carboxy group and an optionally substituted amino group. The cyclopeptides of the invention have high affinity for the KDR receptor of VEGF. The cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of angiogenesis is potentially useful in combating tumour growth, metastasis development, ischaemia, vascular eye diseases and chronic inflammatory disease; and promotion of angiogenesis is potentially useful in promoting tissue regeneration and colonization of implanted biomaterials such as bone substitutes. The present sequence represents a peptide, which is also base don VEGF

XX  
SQ Sequence 7 AA;

Query Match 58.1%; Score 25; DB 5; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.8e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7  
|::||  
Db 2 RIKPH 6

RESULT 7

ABB77935

ID ABB77935 standard; peptide; 7 AA.

XX  
AC ABB77935;

XX  
DT 22-OCT-2002 (first entry)

XX  
DE Amino acid sequence of VEGF-based peptide P3.

XX  
KW Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor; angiogenesis; tumour growth; metastasis development; ischaemia; vascular eye disease; chronic inflammatory disease; tissue regeneration.

XX  
OS Synthetic.

FH Key Location/Qualifiers

FT Modified-site 1 /note= "H attached"

FT Modified-site 7 /note= "OH attached"

FT  
XX  
PN FR2814744-A1.

XX  
PD 05-APR-2002.

XX  
PF 04-OCT-2000; 2000FR-00012654.

XX  
PR 04-OCT-2000; 2000FR-00012654.

XX  
PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.

PA (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.

PA (UYBO-) UNIV BORDEAUX 1.

XX  
PI Betz N, Bikfalvi A, Deleris G;

XX  
DR WPI; 2002-502486/54.

XX  
PT New cyclopeptides containing heptapeptide moiety acting as ligand for the KDR receptor of vascular endothelial growth factor (VEGF), useful, optionally in supported form, as angiogenesis inhibitors or activators.

XX  
PS Disclosure; Page 42; 66pp; French.

XX  
CC The specification describes cyclopeptides, which contain a peptide growth factor (VEGF) which is based on a partial sequence of vascular endothelial growth factor (VEGF). The arginine and glycine residues of ABB77919 are preferably linked by a chain of one or more compounds selected from natural or synthetic amino acids and organic compounds have a carboxy



CC group and an optionally substituted amino group. The cyclopeptides of the  
 CC invention have high affinity for the KDR receptor of VEGF. The  
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of  
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of  
 CC angiogenesis is potentially useful in combating tumour growth, metastasis  
 CC development, ischaemia, vascular eye diseases and chronic inflammatory  
 CC diseases; and promotion of angiogenesis is potentially useful in  
 CC promoting tissue regeneration and colonization of implanted biomaterials  
 CC such as bone substitutes. The present sequence represents a peptide,  
 CC which is also base don VEGF

XX SQ Sequence 7 AA;

Query Match 58.1%; Score 25; DB 5; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RVRPH 7  
 |::||  
 Db 1 RIKPH 5

#### RESULT 8

ABE77926  
 ID ABE77926 standard; peptide; 7 AA.

XX AC ABE77926;

XX 22-OCT-2002 (first entry)

DE Amino acid sequence of cyclopeptide P16 based on VEGF.

XX Cyclopeptide; vascular endothelial growth factor; VEGF; KDR receptor;  
 KW angiogenesis; tumour growth; metastasis development; ischaemia;  
 KW vascular eye disease; chronic inflammatory disease; tissue regeneration.  
 XX Synthetic.

XX FR2814744-A1.

XX 05-APR-2002.

XX 04-OCT-2000; 2000FR-00012654.

XX 04-OCT-2000; 2000FR-00012654.

PA (COMS ) COMMISSARIAT ENERGIE ATOMIQUE.

PA (UYBO-) UNIV BORDEAUX 2 SEGALLEN VICTOR.

PA (UYBO-) UNIV BORDEAUX 1.

XX Betz N, Birkfalvi A, Deleris G;

XX WPI; 2002-502486/54.

XX New cyclopeptides containing heptapeptide moiety acting as ligand for the  
 PT KDR receptor of vascular endothelial growth factor (VEGF), useful,  
 PT optionally in supported form, as angiogenesis inhibitors or activators.

XX Claim 3; Page 44; 66pp; French.

XX The present sequence represents a cyclopeptide, which contains a peptide  
 CC (ABB77919) which is based on a partial sequence of vascular endothelial  
 CC growth factor (VEGF). The arginine and glycine residues of ABB77919 are  
 CC preferably linked by a chain of one or more compounds selected from  
 CC natural or synthetic amino acids and organic compounds have a carboxy  
 CC group and an optionally substituted amino group. The cyclopeptides of the  
 CC invention have high affinity for the KDR receptor of VEGF. The  
 CC cyclopeptides mediate in angiogenesis by bonding to the KDR receptor of  
 CC VEGF, and can be used to inhibit or promote angiogenesis. Inhibition of  
 CC angiogenesis is potentially useful in combating tumour growth, metastasis  
 CC development, ischaemia, vascular eye diseases and chronic inflammatory  
 CC diseases; and promotion of angiogenesis is potentially useful in  
 CC promoting tissue regeneration and colonization of implanted biomaterials

CC such as bone substitutes  
 XX SQ Sequence 7 AA;

Query Match 58.1%; Score 25; DB 5; Length 7;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 RVRPH 7  
 |::||  
 Db 1 RIKPH 5

#### RESULT 9

AAR83529

ID AAR83529 standard; protein; 6 AA.

XX AC AAR83529;

XX 23-APR-1996 (first entry)

DE Zif268 zinc finger 2 randomised residues with affinity for HIV-1.

XX zinc finger; variant; randomised; alpha-helical region; Zif268;  
 KW customised affinity; cancer; therapy; virus infection; HIV-1;  
 KW human immunodeficiency virus; consensus target sequence;  
 KW transcription-activator; transcription-inhibitor; plant disease.

XX OS Synthetic.

XX PN WO9519431-A1.

XX 20-JUL-1995.

XX 18-JAN-1995; 95WO-US0000829.

XX 18-JAN-1994; 94US-00183119.

XX 28-SEP-1994; 94US-00312604.

XX (SCRI ) SCRIPPS RES INST.

XX Barbas CF, Gottesfeld JM, Wright PE;

XX WPI; 1995-263862/34.

XX New zinc finger-nucleotide binding polypeptide(s) - used for modulating  
 PT the function of cellular nucleotide sequences, partic. for treating cell  
 PT proliferative disorders.

XX Example 10; Fig 9; 135pp; English.

XX Regions of the alpha-helix in each of the Zif268 zinc fingers 1, 2 and 3  
 CC were randomised and selected for binding to particular conserved target  
 CC sequences in HIV-1. In finger 2, the randomised residues were at  
 CC positions -2,-1,1,2,3 and 4 in the alpha-helical region. The present  
 CC sequence has affinity for the TGG target sequence. Zinc finger proteins  
 CC are useful for suppressing transcription and therefore for treating  
 CC proliferative disorders

XX SQ Sequence 6 AA;

Query Match 55.8%; Score 24; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VRPH 7  
 |::||  
 Db 1 VRPH 4

#### RESULT 10

AAW84427

ID AAW84427 standard; peptide; 6 AA.

XX AAW84427;  
 AC  
 XX  
 DT 22-MAR-1999 (first entry)  
 DE  
 XX HTV-1 nucleic acid binding protein zinc finger 2 peptide.  
 KW zinc finger; nucleotide-binding protein; cell proliferative disorder;  
 KW gene therapy; cancer; psoriasis; pemphigus vulgaris; Bechet's syndrome;  
 KW lipid histiocytosis; human immune deficiency virus; HIV; viral infection;  
 KW transgenic plant.  
 XX  
 OS Synthetic.  
 XX  
 XX WO9854311-A1.  
 PN  
 XX  
 PD 03-DEC-1998.  
 XX  
 XX 27-MAY-1998; 98WO-US010801.  
 PF  
 XX 27-MAY-1997; 97US-00863813.  
 PR  
 XX (SCRI ) SCRIPPS RES INST.  
 PA  
 XX Barbas CP, Gottesfeld JM, Wright PE;  
 PI WPI; 1999-059831/05.  
 DR  
 XX  
 XX New zinc finger nucleotide-binding protein variant that modulates  
 PT selected nucleotide sequence - used for treatment of proliferative and  
 PT viral diseases by gene therapy, and can be made selective for any target  
 PT sequence.  
 XX  
 XX Example 10; Fig 9; 158pp; English.  
 PS  
 XX  
 CC AAW84422-41 represent the peptides obtained from randomised finger 2  
 CC sequences of zinc finger nucleotide-binding proteins that bind to HIV-1  
 CC target sequences. The peptides were produced in the course of the  
 CC invention. The specification describes zinc finger nucleotide-binding  
 CC protein variants with at least two zinc finger modules that bind to a  
 CC cellular nucleotide sequence and modulate its function. Zinc finger  
 CC proteins, and compositions containing them, are used to increase or  
 CC reduce transcription of a gene linked to the cellular nucleotide  
 CC sequence. The proteins are used specifically for treating or preventing  
 CC cell proliferative disorders (in humans, animals or plants, including  
 CC those induced by viruses), particularly where expressed from nucleic acid  
 CC by gene therapy (including ex vivo methods). Typical diseases that can be  
 CC treated are many forms of cancer, psoriasis, pemphigus vulgaris, Bechet's  
 CC syndrome and lipid histiocytosis, also treatment of human immune  
 CC deficiency virus (HIV) and other viral infections, and production of  
 CC transgenic plants resistant to bacterial and viral diseases. The present  
 CC oligonucleotide is used in the course of the invention  
 XX  
 SQ Sequence 6 AA;  
 Query Match 55.8%; Score 24; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4 VRPH 7  
 DB 1 VRPH 4  
 RESULT 11  
 AAB14509  
 ID AAB14509 standard; peptide; 6 AA.  
 AC AAB14509;  
 XX  
 XX 14-NOV-2000 (first entry)  
 DT  
 XX Sterile alpha motif (SAM) domain peptide, SEQ ID NO:110.

XX SAM domain; sterile alpha motif; homodimerisation; heterodimerisation;  
 KW signal transduction; X-ray crystallography; protein coordinate data;  
 KW drug development; antibody; T-cell signalling; telomere function;  
 KW cell proliferative disorder; senescence; ageing; cancer; atherosclerosis;  
 KW arthritis; angiogenesis; neuronal development; axonal migration;  
 KW neurodegeneration; neurodegenerative disease; Alzheimer's disease;  
 KW Parkinson's disease; Huntington's disease; demyelinating disease;  
 KW multiple sclerosis; amyotrophic lateral sclerosis; nervous system trauma;  
 KW stroke; ischaemia; cytotoxic; immunosuppressive; vulnerary;  
 KW neuroprotective; neurotropic; antiparkinsonian; cerebroprotective;  
 KW antiarthritic; antiatherosclerotic.  
 XX  
 OS Unidentified.  
 XX  
 XX WO200037500-A1.  
 PN  
 XX 29-JUN-2000.  
 PD  
 XX 17-DEC-1999; 99WO-CA001209.  
 PF  
 XX 18-DEC-1998; 98US-0112929P.  
 PR  
 XX (MOUN ) MOUNT SINAI HOSPITAL.  
 PA  
 XX Stapleton D, Sicheri F;  
 PI WPI; 2000-442645/38.  
 DR  
 XX 3-D structure of sterile alpha motif domain used as model for determining  
 PT 3-D structures of additional native or mutated SAM domain with unknown  
 PT structure and structures of co-crystals of SAM domain with modulators.  
 XX  
 PS Claim 24; Page 48; 72pp; English.  
 XX  
 CC The invention relates to the three dimensional structure of a SAM (sterile  
 CC alpha motif) domain, to peptides (AAB14420-B14525) which mediate SAM  
 CC domain function, and to potential modulators of SAM domain function. The  
 CC SAM domain mediates homo- and heterodimerisation and is found in cell  
 CC surface receptors, cytoplasmic signalling proteins, transcriptional  
 CC activators and repressors and chimeric human oncoproteins. For example it  
 CC is present in the Eph family of receptor tyrosine kinases, the  
 CC transcription factor TEL, members of the polycomb group of  
 CC transcriptional repressors (e.g., RAE28, Scm), the protein kinase Bcr2p  
 CC and liprin scaffolding proteins. SAM domains are therefore thought to  
 CC play an important role in both normal and oncogenic signal transduction.  
 CC The X-ray crystal structure was determined for the SAM domain of the  
 CC murine ephrin A receptor isoform EphA4 (AAB14400; also known as Sek,  
 CC Sek1, Cck8, Hek8, and Tyrol1). The SAM domain corresponds to residues 890-  
 CC 981 of EphA4. The 3D structure of the SAM domain can be used in the  
 CC determination of the structures of other SAM domain-containing proteins.  
 CC The SAM domain peptides may be used to identify compounds for drug  
 CC development and to prepare antibodies. The antibodies can be used to  
 CC screen for SAM domain-containing proteins, to diagnose and treat  
 CC disorders associated with aberrant T-cell signalling, and to modulate  
 CC telomere function. Modulators of SAM domain function may be used to treat  
 CC diseases associated with inappropriate activity of a protein containing a  
 CC SAM domain, particularly an Eph receptor. They may be used to treat a  
 CC cell proliferative disorder such as cancer, atherosclerosis, arthritis  
 CC and diseases associated with the nervous system, and may be used to  
 CC modulate angiogenesis. The SAM domain peptides and modulators may be used  
 CC to modulate the biological activity of an Eph receptor or Eph ligand in a  
 CC cell, particularly in pathways involved in neuronal development, axonal  
 CC migration, pathfinding and regeneration. Compositions containing SAM  
 CC domain modulators may be used in the treatment of neurodegenerative  
 CC diseases (e.g., Alzheimer's disease, Parkinson's disease, Huntington's  
 CC disease, demyelinating diseases such as multiple sclerosis, and  
 CC amyotrophic lateral sclerosis) and conditions involving trauma and injury  
 CC to the nervous system (e.g., ischaemia resulting from stroke, and  
 CC bacterial and viral infection of the nervous system). Sequences AAB14420-  
 CC B14525 represent peptides which mediate SAM domain function  
 XX  
 XX Sequence 6 AA;

Query Match 55.8%; Score 24; DB 3; Length 6;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HGRVRP 6  
 Db 1 HGRMVP 6

## RESULT 12

ABP98596  
 ID ABP98596 standard; peptide; 7 AA.

XX AC ABP98596;

XX 18-SEP-2003 (first entry)

XX Clone #3 from peptide library.

XX Peptide library; cytostatic; tumour cell growth inhibitor;  
 XX Transcription factor E2F inhibitor; cell duplication; clone.

XX Unidentified.

XX WO2003051312-A2.

XX 26-JUN-2003.

XX 17-DEC-2002; 2002WO-US040355.

XX 18-DEC-2001; 2001US-0341908P.

XX (SLOK) SLOAN KETTERING INST CANCER RES.

XX Scarborough AL, Banerjee D, Bertino JR;

XX WPI; 2003-569108/53.

XX Composition useful for inhibiting of tumor cell growth comprises an amino acid peptide or its derivative.

XX Disclosure; Page 19; 32pp; English.

XX This invention relates to an amino acid peptide believed to be cytostatic in its action used as a tumour cell growth inhibitor and a transcription factor E2F inhibitor. The peptides can be used for inhibiting tumour cell growth and the activity of transcription factor E2F. The compounds inhibit the transcription factor E2F produced by the phosphorylation of the tumour suppressor pRb gene by cyclinD/CDK activities, and the subsequent cell duplication. The present sequence represents a clone from the random peptide library. Present in the exemplification of the specification

XX Sequence 7 AA;

Query Match 55.8%; Score 24; DB 7; Length 7;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 HGRVRPH 7  
 Db 1 HAIVRPH 7

## RESULT 13

AAW74241  
 ID AAW74241 standard; peptide; 7 AA.

XX AC AAW74241;

XX 05-MAY-1999 (first entry)

DE HJ loop peptide HJ13.

XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;  
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;  
 KW inflammatory disorder; central nervous system disease; septic shock;  
 KW Parkinson's disease; hypertension.

XX Synthetic.

XX Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"

FT Modified-site 7 /note= "amidated"

XX WO9853051-A1.

XX 26-NOV-1998.

XX 20-MAY-1998; 98WO-US010321.

XX 21-MAY-1997; 97US-00861153.

XX (CHIL-) CHILDRENS MEDICAL CENT.

XX Ben-Sasson SA;

XX WPI; 1999-070143/06.

XX New peptide derivatives for modulating protein tyrosine kinase activity - comprise a sequence corresponding to the HJ loop of a protein tyrosine kinase, used for treating cancers or immune disorders.

XX Claim 20; Fig 3; 79pp; English.

XX This sequence represents a peptide of the invention, and is a derivative of the HJ loop of a serine/threonine kinase (STK). The peptides can be used for the treatment of disorders caused by overactivity or underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis, arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and hypertension), immunosuppressive and inflammatory disorders (e.g. asthma, psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression of organ transplant rejection, multiple sclerosis, inflammatory bowel disease and AIDS), central nervous system diseases (e.g. Alzheimer's disease, stroke and trauma), septic shock, Parkinson's disease or hypertension. The peptides can also be used to produce antibodies which can be used to identify cells expressing the STK and to study the intracellular distribution of the STK. In addition, the peptides can be used to identify and quantitate ligands which bind the HJ loop of the STK from which the peptide was derived

XX Sequence 7 AA;

Query Match 53.5%; Score 23; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGRV 4  
 Db 4 HGRV 7

## RESULT 14

AAW87203  
 ID AAW87203 standard; peptide; 6 AA.

XX AC AAW87203;

XX 09-FEB-1999 (first entry)

XX Peptide determined by the method of the invention.

KW Amino acid determination; molecular mass; fragmentation spectrum;  
 XX DNA cloning; anti-body; recombinant; modification; mass spectrometry.  
 OS Synthetic.  
 XX  
 XX GB2325465-A.  
 XX  
 XX 25-NOV-1998.  
 XX  
 XX 22-MAY-1998; 98GB-00011196.  
 XX  
 XX 22-MAY-1997; 97GB-00010582.  
 XX  
 XX (OXFO-) OXFORD GLYSCSCIENCES UK LTD.  
 XX  
 XX Parekh RB, Prime SB, Wedd NS, Townsend RR;  
 XX  
 XX WPI; 1998-571195/49.  
 XX  
 XX Peptide sequence determination used in e.g. DNA cloning - by comparing  
 PT mass spectra of the unknown peptide with a library of linear chain known  
 PT peptide sequences.  
 XX  
 XX Example 1; Page 21; 40pp; English.  
 XX  
 XX The invention relates to a method for determination of the amino acid  
 CC sequence of an unknown peptide. The method comprises (a) determining the  
 CC molecular mass and an experimental fragmentation spectrum for the peptide  
 CC ; (b) comparing the experimental fragmentation spectrum of the unknown  
 CC peptide with a theoretical fragmentation spectra calculated for a peptide  
 CC library composed of all possible linear sequences of amino acids having a  
 CC total mass that corresponds to the molecular mass of the unknown peptide;  
 CC and (c) identifying a peptide in the library with a theoretical  
 CC fragmentation spectrum that most closely matches the fragmentation  
 CC spectrum of the unknown peptide. The method is useful in DNA cloning,  
 CC anti-body production, identification of recombinant products, and the  
 CC study of post-translational modifications. It allows the sequence of  
 CC unknown peptides or proteins with no sub-sequence identity, to be  
 CC characterised using mass spectrometry. Sequences AAW87101 to AAW87364  
 CC represent a library of linear peptides constructed to exemplify the  
 CC method. The isoleucine residue in these peptides can be replaced by  
 CC leucine to construct another 264 linear peptides to be included in the  
 XX library  
 XX  
 XX Sequence 6 AA;  
 SQ  
 Query Match 51.2%; Score 22; DB 2; Length 6;  
 Best Local Similarity 60.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 HGRVR 5  
 DB |||:  
 2 HGEIR 6  
 RESULT 15  
 AAW74242  
 ID AAW74242 standard; peptide; 7 AA.  
 XX  
 XX AAW74242;  
 XX  
 XX 05-MAY-1999 (first entry)  
 XX  
 XX HJ loop peptide HJ23.1.  
 DE  
 XX  
 XX HJ loop; serine/threonine kinase; cancer; diabetes; obesity; therapy;  
 KW haemorrhagic shock; cardiovascular disease; immunosuppressive disorder;  
 KW inflammatory disorder; central nervous system disease; septic shock;  
 KW Parkinson's disease; hypertension.  
 XX  
 XX Synthetic.  
 OS  
 XX  
 XX Key Location/Qualifiers

FT Modified-site 1 /note= "acetylated"  
 FT Modified-site 7 /note= "amidated"  
 FT  
 XX  
 XX MO9853051-A1.  
 XX  
 XX 26-NOV-1998.  
 XX  
 XX 20-MAY-1998; 98WO-US010321.  
 XX  
 XX 21-MAY-1997; 97US-00861153.  
 XX  
 XX (CHIL-) CHILDRENS MEDICAL CENT.  
 XX  
 XX Ben-Sasson SA;  
 XX  
 XX WPI; 1999-070143/06.  
 XX  
 XX New peptide derivatives for modulating protein tyrosine kinase activity -  
 PT comprise a sequence corresponding to the HJ loop of a protein tyrosine  
 PT kinase, used for treating cancers or immune disorders.  
 XX  
 XX Claim 20; Fig 3; 79pp; English.  
 XX  
 XX This sequence represents a peptide of the invention, and is a derivative  
 CC of the HJ loop of a serine/threonine kinase (STK). The peptides can be  
 CC used for the treatment of disorders caused by overactivity or  
 CC underactivity of a STK, e.g. cancer, diabetes, obesity, haemorrhagic  
 CC shock, cardiovascular diseases (e.g. thrombosis, atherosclerosis,  
 CC arteriosclerosis, cardiac hyper trophy, ischaemia, reperfusion injury and  
 CC hypertension), immunosuppressive and inflammatory disorders (e.g. asthma,  
 CC psoriasis, systemic lupus erythematosus, diabetes mellitus, suppression  
 CC of organ transplant rejection, multiple sclerosis, inflammatory bowel  
 CC disease and AIDS), central nervous system diseases (e.g. Alzheimer's  
 CC disease, stroke and trauma), septic shock, Parkinson's disease or  
 CC hypertension. The peptides can also be used to produce antibodies which  
 CC can be used to identify cells expressing the STK and to study the  
 CC intracellular distribution of the STK. In addition, the peptides can be  
 CC used to identify and quantitate ligands which bind the HJ loop of the STK  
 CC from which the peptide was derived  
 XX  
 XX Sequence 7 AA;  
 SQ  
 Query Match 51.2%; Score 22; DB 2; Length 7;  
 Best Local Similarity 75.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 HGRV 4  
 DB |||:  
 4 HGRI 7  
 Search completed: August 3, 2005, 12:03:10  
 Job time : 99.3333 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 25 Seconds  
(without alignments)

20.902 Million cell updates/sec

Title: US-09-910-582B-3

Perfect score: 43

Sequence: 1 HGRVRPH 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 61165

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:\*

1: /cgn2\_6/ptodata/1/iaa/5A COMB.pap:\*

2: /cgn2\_6/ptodata/1/iaa/5B COMB.pap:\*

3: /cgn2\_6/ptodata/1/iaa/6A COMB.pap:\*

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5: /cgn2\_6/ptodata/1/iaa/6C COMB.pap:\*

6: /cgn2\_6/ptodata/1/iaa/backfilea1.pap:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	43	100.0	7	3	US-09-326-718-3
2	24	55.8	6	4	US-09-500-700-101
3	23	53.5	7	4	US-08-861-153A-26
4	22	51.2	6	4	US-08-877-605-103
5	22	51.2	7	4	US-09-202-329-21
6	22	51.2	7	4	US-08-861-153A-34
7	21	48.8	5	4	US-08-839-743-27
8	20	46.5	4	2	US-08-177-109A-22
9	20	46.5	4	2	US-08-687-706-22
10	20	46.5	6	1	US-08-225-224-53
11	20	46.5	6	3	US-08-722-258-53
12	20	46.5	6	3	US-09-196-934-4
13	20	46.5	6	4	US-08-877-605-116
14	20	46.5	6	5	PCT-US95-04468-53
15	20	46.5	7	1	US-08-074-210-3
16	20	46.5	7	1	US-08-074-210-5
17	20	46.5	7	2	US-08-177-109A-55
18	20	46.5	7	2	US-08-687-706-55
19	20	46.5	7	3	US-09-139-802-85
20	20	46.5	7	3	US-09-025-819-3
21	20	46.5	7	3	US-09-031-902-5
22	20	46.5	7	3	US-09-031-902-6
23	20	46.5	7	3	US-09-031-902-11
24	20	46.5	7	3	US-09-031-902-12
25	20	46.5	7	4	US-09-808-126-3
26	20	46.5	7	4	US-09-803-951-3
27	20	46.5	7	4	US-09-659-786-85

28	46.5	7	4	US-08-926-914-85	Sequence 85, Appl
29	46.5	7	5	PCT-US94-06502A-4	Sequence 4, Appl
30	46.5	7	5	PCT-US94-06502A-5	Sequence 5, Appl
31	44.2	4	4	US-10-132-920B-52	Sequence 52, Appl
32	44.2	4	4	US-09-700-696C-49	Sequence 49, Appl
33	44.2	5	2	US-08-350-260A-410	Sequence 410, App
34	44.2	5	4	US-08-055-006-47	Sequence 47, Appl
35	44.2	5	4	US-09-104-337A-410	Sequence 410, App
36	44.2	6	1	US-08-665-220-18	Sequence 18, Appl
37	44.2	6	2	US-08-618-408B-18	Sequence 18, Appl
38	44.2	6	2	US-08-893-853-13	Sequence 13, Appl
39	44.2	6	3	US-09-113-921-13	Sequence 13, Appl
40	44.2	6	3	US-09-257-218-29	Sequence 29, Appl
41	44.2	6	3	US-09-311-760-29	Sequence 29, Appl
42	44.2	6	3	US-09-291-692-18	Sequence 18, Appl
43	44.2	6	3	US-09-561-756-67	Sequence 67, Appl
44	44.2	6	3	US-09-227-721-67	Sequence 67, Appl
45	44.2	6	4	US-09-155-613A-44	Sequence 44, Appl
46	44.2	6	4	US-08-865-579-29	Sequence 29, Appl
47	44.2	6	4	US-09-451-067-13	Sequence 13, Appl
48	44.2	6	4	US-10-059-749-29	Sequence 29, Appl
49	44.2	6	4	US-08-877-605-31	Sequence 31, Appl
50	44.2	6	4	US-08-877-605-32	Sequence 32, Appl
51	44.2	6	4	US-08-877-605-33	Sequence 33, Appl
52	44.2	6	4	US-08-877-605-34	Sequence 34, Appl
53	44.2	6	4	US-08-877-605-35	Sequence 35, Appl
54	44.2	6	4	US-08-877-605-36	Sequence 36, Appl
55	44.2	6	4	US-09-954-697-67	Sequence 67, Appl
56	44.2	6	4	US-09-352-768-18	Sequence 18, Appl
57	44.2	7	2	US-08-726-306A-20	Sequence 20, Appl
58	44.2	7	4	US-09-007-288B-48	Sequence 48, Appl
59	41.9	6	4	US-08-877-605-127	Sequence 127, App
60	40.7	5	6	5217869-57	Patent No. 5217869
61	40.7	5	6	5217869-57	Patent No. 5217869
62	39.5	5	1	US-08-467-940-2	Sequence 2, Appl
63	39.5	5	1	US-08-633-772-2	Sequence 2, Appl
64	39.5	5	1	US-08-259-550A-24	Sequence 24, Appl
65	39.5	5	3	US-08-871-572B-17	Sequence 17, Appl
66	39.5	6	1	US-08-037-486-4	Sequence 4, Appl
67	39.5	6	1	US-08-014-979-93	Sequence 93, Appl
68	39.5	6	1	US-08-249-371-6	Sequence 6, Appl
69	39.5	6	1	US-08-259-550A-3	Sequence 3, Appl
70	39.5	6	3	US-09-135-021-74	Sequence 74, Appl
71	39.5	6	3	US-08-218-369-3	Sequence 3, Appl
72	39.5	6	4	US-09-155-613A-75	Sequence 75, Appl
73	39.5	6	4	US-08-877-605-141	Sequence 141, App
74	39.5	6	4	US-09-904-599A-3	Sequence 3, Appl
75	39.5	6	5	PCT-US95-03742-3	Sequence 3, Appl
76	39.5	6	5	PCT-US95-06451-6	Sequence 6, Appl
77	39.5	7	1	US-07-977-234C-9	Sequence 9, Appl
78	39.5	7	1	US-08-366-276-4	Sequence 4, Appl
79	39.5	7	1	US-08-346-333-86	Sequence 86, Appl
80	39.5	7	1	US-08-259-550A-25	Sequence 25, Appl
81	39.5	7	1	US-08-259-550A-26	Sequence 26, Appl
82	39.5	7	1	US-08-259-550A-45	Sequence 45, Appl
83	39.5	7	3	US-08-640-737-35	Sequence 35, Appl
84	39.5	7	3	US-09-031-902-8	Sequence 8, Appl
85	39.5	7	4	US-09-485-534-5	Sequence 5, Appl
86	39.5	7	5	PCT-US91-07506-86	Sequence 86, Appl
87	37.2	3	1	US-08-037-486-11	Sequence 11, Appl
88	37.2	4	1	US-08-037-486-5	Sequence 5, Appl
89	37.2	4	1	US-08-259-550A-4	Sequence 4, Appl
90	37.2	4	2	US-08-244-496-35	Sequence 35, Appl
91	37.2	4	2	US-08-244-496-47	Sequence 47, Appl
92	37.2	5	2	US-08-244-496-51	Sequence 51, Appl
93	37.2	5	2	US-08-348-353-8	Sequence 8, Appl
94	37.2	5	3	US-08-465-965-8	Sequence 8, Appl
95	37.2	5	3	US-08-465-966-8	Sequence 8, Appl
96	37.2	5	3	US-09-298-924-42	Sequence 42, Appl
97	37.2	6	1	US-09-459-958-9	Sequence 9, Appl
98	37.2	6	1	US-08-014-979-75	Sequence 75, Appl
99	37.2	6	1	US-08-014-979-77	Sequence 77, Appl
100	37.2	6	1	US-08-471-052A-164	Sequence 164, App

## ALIGNMENTS

RESULT 1  
US-09-326-718-3  
; Sequence 3, Application US/09326718  
; Patent No. 6303573  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: MacKenna, Deirdre A.  
; TITLE OF INVENTION: Heart Homing Peptides and Methods of  
; TITLE OF INVENTION: Using Same  
; FILE REFERENCE: P-LJ 3512  
; CURRENT APPLICATION NUMBER: US/09/326,718  
; CURRENT FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-326-718-3  
  
Query Match 100.0%; Score 43; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGRVRPH 7  
Db 1 HGRVRPH 7

RESULT 2  
US-09-500-700-101  
; Sequence 101, Application US/09500700  
; Patent No. 6790941  
; GENERAL INFORMATION:  
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE  
; APPLICANT: BARBAS III, Carlos F.  
; APPLICANT: GOTTESFELD, Joel M.  
; APPLICANT: WRIGHT, Peter E.  
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR  
; FILE REFERENCE: SCRIPI160-4  
; CURRENT APPLICATION NUMBER: US/09/500,700  
; CURRENT FILING DATE: 2003-01-10  
; PRIOR APPLICATION NUMBER: US 08/863,813  
; PRIOR FILING DATE: 1997-05-27  
; PRIOR APPLICATION NUMBER: US 08/676,318  
; PRIOR FILING DATE: 1996-12-30  
; PRIOR APPLICATION NUMBER: PCT/US95/00829  
; PRIOR FILING DATE: 1995-01-18  
; PRIOR APPLICATION NUMBER: US 08/312,604  
; PRIOR FILING DATE: 1994-09-28  
; PRIOR APPLICATION NUMBER: US 08/183,119  
; PRIOR FILING DATE: 1994-01-18  
; NUMBER OF SEQ ID NOS: 127  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 101  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Modified sequence of finger 2 of zif268  
US-09-500-700-101  
  
Query Match 55.8%; Score 24; DB 4; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VRPH 7  
Db 1 VRPH 4

RESULT 3  
US-08-861-153A-26  
; Sequence 26, Application US/08861153A  
; Patent No. 6723694  
; GENERAL INFORMATION:  
; APPLICANT: BEN-SASSON, Shmuel A  
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY MODULATE INTRACELLULAR SIGNALING  
; FILE REFERENCE: BEN-SASSON-1  
; CURRENT APPLICATION NUMBER: US/08/861,153A  
; CURRENT FILING DATE: 1997-05-21  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 26  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: MOD RES  
; LOCATION: (1)-(1)  
; OTHER INFORMATION: N-Acetyl-Leucine  
; NAME/KEY: MOD RES  
; LOCATION: (7)-(7)  
; OTHER INFORMATION: Valine-NH2  
US-08-861-153A-26  
  
Query Match 53.5%; Score 23; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 HGRV 4  
Db 4 HGRV 7

RESULT 4  
US-08-877-605-103  
; Sequence 103, Application US/08877605  
; Patent No. 6582965  
; GENERAL INFORMATION:  
; APPLICANT: Robert Townsend  
; APPLICANT: Raj Parekh  
; APPLICANT: Sally Prime  
; APPLICANT: Nick Webb  
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION  
; FILE REFERENCE: 9195-004  
; CURRENT APPLICATION NUMBER: US/08/877,605  
; CURRENT FILING DATE: 1997-06-18  
; NUMBER OF SEQ ID NOS: 353  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 103  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Peptide X Library  
US-08-877-605-103  
  
Query Match 51.2%; Score 22; DB 4; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HGRVR 5  
Db 2 HGEIR 6

RESULT 5

US-09-202-329-21  
; Sequence 21, Application US/09202329A  
; Patent No. 6676944  
; GENERAL INFORMATION:  
; APPLICANT: Dalton, John P  
; APPLICANT: Andrews, Stuart J  
; TITLE OF INVENTION: Vaccine containing a peroxiredoxin and/or a B-tubulin  
; FILE REFERENCE: 1181-243  
; CURRENT APPLICATION NUMBER: US/09/202,329A  
; PRIOR FILING DATE: 1999-02-19  
; EARLIER APPLICATION NUMBER: GB 9612214.8  
; EARLIER FILING DATE: 1996-06-11  
; EARLIER APPLICATION NUMBER: PCT/GB97/01573  
; EARLIER FILING DATE: 1997-06-11  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Fasciola hepatica  
US-09-202-329-21

Query Match 51.2%; Score 22; DB 4; Length 7;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
QY 1 HGRVVP 6  
Db 1 HGEVCP 6

RESULT 6  
US-08-861-153A-34  
; Sequence 34, Application US/08861153A  
; Patent No. 6723694  
; GENERAL INFORMATION:  
; APPLICANT: BEN-SASSON, Shmuel A  
; TITLE OF INVENTION: SHORT PEPTIDES WHICH SELECTIVELY MODULATE INTRACELLULAR SIGNALING  
; FILE REFERENCE: BEN-SASSON=1  
; CURRENT APPLICATION NUMBER: US/08/861,153A  
; CURRENT FILING DATE: 1997-05-21  
; NUMBER OF SEQ ID NOS: 53  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 34  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic  
; NAME/KEY: MOD RES  
; LOCATION: (1)..(1)  
; OTHER INFORMATION: N-Acetyl-Isoleucine  
; NAME/KEY: MOD RES  
; LOCATION: (7)..(7)  
; OTHER INFORMATION: Isoleucine-NH2  
US-08-861-153A-34

Query Match 51.2%; Score 22; DB 4; Length 7;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 1 HGRV 4  
Db 4 HGRI 7

RESULT 7  
US-09-839-743-27  
; Sequence 27, Application US/09839743  
; Patent No. 6472211  
; GENERAL INFORMATION:  
; APPLICANT: The Salk Institute for Biological Sciences  
; APPLICANT: Lamb, Christopher

; APPLICANT: Doerner, Peter  
; APPLICANT: Laible, Goetz  
; TITLE OF INVENTION: No. 6472211el Transcription Enhancer Element and  
; FILE REFERENCE: Transcription Factor and Methods of Use Thereof  
; FILE REFERENCE: SALKINS.008DV3  
; CURRENT APPLICATION NUMBER: US/09/839,743  
; CURRENT FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: US 09/401,336  
; PRIOR FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: US 09/189,344  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 08/669,721  
; PRIOR FILING DATE: 1996-06-27  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Nicotiana tabacum  
US-09-839-743-27

Query Match 48.8%; Score 21; DB 4; Length 5;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 GRVVP 6  
Db 1 GRPRP 5

RESULT 8  
US-08-177-109A-22  
; Sequence 22, Application US/08177109A  
; Patent No. 5863615  
; GENERAL INFORMATION:  
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; STREET: 1201 West Peachtree Street  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/177,109A  
; FILING DATE: 03-JAN-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: WU 107  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
US-08-177-109A-22

Query Match 46.5%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPH 7  
Db 1 RPH 3

## RESULT 9

US-08-687-706-22  
; Sequence 22, Application US/08687706  
; Patent No. 5928892  
; GENERAL INFORMATION:  
; APPLICANT: Dennis E. Hourcade and Teresa J. Oglesby  
; TITLE OF INVENTION: MODIFIED COMPLEMENT PROTEASES  
; NUMBER OF SEQUENCES: 62  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Patrea L. Pabst  
; STREET: 2800 One Atlantic Center  
; CITY: Atlanta  
; STATE: Georgia  
; COUNTRY: USA  
; ZIP: 30309-3450  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/687,706  
; FILING DATE: 26-JUL-1996  
; CLASSIFICATION: 514  
; PRIOR APPLICATION NUMBER: US 08/177,109  
; FILING DATE: 03-JAN-1994  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Pabst, Patrea L.  
; REGISTRATION NUMBER: 31,284  
; REFERENCE/DOCKET NUMBER: WU 107 DIV  
; TELEPHONE: (404) 873-8794  
; TELEFAX: (404) 873-8795  
; INFORMATION FOR SEQ ID NO: 22:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 4 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHEICAL: NO

## US-08-687-706-22

Query Match 46.5%; Score 20; DB 2; Length 4;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPH 7  
Db 1 RPH 3

## RESULT 10

US-08-225-224-53  
; Sequence 53, Application US/08225224  
; Patent No. 5635599  
; GENERAL INFORMATION:  
; APPLICANT: PASTAN, Ira  
; APPLICANT: KREITMAN, Robert J.  
; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND  
; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS  
; NUMBER OF SEQUENCES: 57  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew

; STREET: Steuart Street Tower, One Market Plaza  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: US  
; ZIP: 94105-1493  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/225,224  
; FILING DATE: 8-APR-1994  
; CLASSIFICATION: 530  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Weber, Ellen L.  
; REGISTRATION NUMBER: 32,762  
; REFERENCE/DOCKET NUMBER: 15280-193  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 543-9600  
; TELEFAX: (415) 543-5043  
; INFORMATION FOR SEQ ID NO: 53:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: unknown  
; TOPOLOGY: unknown  
; MOLECULE TYPE: peptide

## US-08-225-224-53

Query Match 46.5%; Score 20; DB 1; Length 6;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 RPH 7  
Db 1 RPH 3

## RESULT 11

US-08-722-258-53  
; Sequence 53, Application US/08722258  
; Patent No. 6011002  
; GENERAL INFORMATION:  
; APPLICANT: Pastan, Ira  
; APPLICANT: Kreitman, Robert J.  
; APPLICANT: Puri, Raj K.  
; TITLE OF INVENTION: Circularly Permuted Ligands and  
; TITLE OF INVENTION: Circularly Permuted Chimeric Molecules  
; NUMBER OF SEQUENCES: 72  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend and Crew LLP  
; STREET: Two Embarcadero Center, Eighth Floor  
; CITY: San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94111-3834  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/722,258  
; FILING DATE: 08-JAN-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: WO PCT/US95/04468  
; FILING DATE: 08-APR-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/225,224  
; FILING DATE: 08-APR-1994  
; ATTORNEY/AGENT INFORMATION:



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; NAME: Weber, Ellen Lauver
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 015280-193100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-722-258-53

Query Match 46.5%; Score 20; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RPH 7
Db 1 RPH 3

RESULT 12
US-09-196-934-4
; Sequence 4, Application US/09196934
; Patent No. 6191256
; GENERAL INFORMATION:
; APPLICANT: Chen, Li Ang
; APPLICANT: Beutner, Joseph A.
; APPLICANT: Carbone, Ruben G.
; TITLE OF INVENTION: Recombinant Factor VIII Binding Peptides
; FILE REFERENCE: MSB-7251
; CURRENT APPLICATION NUMBER: US/09/196,934
; CURRENT FILING DATE: 1998-11-20
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-196-934-4

Query Match 46.5%; Score 20; DB 3; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RPH 7
Db 2 RPH 4

RESULT 13
US-08-877-605-116
; Sequence 116, Application US/08877605
; Patent No. 6582965
; GENERAL INFORMATION:
; APPLICANT: Robert Townsend
; APPLICANT: Raj Parekh
; APPLICANT: Sally Prime
; APPLICANT: Nick Webb
; TITLE OF INVENTION: A METHOD FOR DE NOVO PEPTIDE SEQUENCE DETERMINATION
; FILE REFERENCE: 9195-004
; CURRENT APPLICATION NUMBER: US/08/877,605
; CURRENT FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 353
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 116
; LENGTH: 6
; TYPE: PRT
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; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide X Library
US-08-877-605-116

Query Match 46.5%; Score 20; DB 4; Length 6;
Best Local Similarity 60.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 HGRVR 5
Db 2 HGHIR 6

RESULT 14
PCT-US95-04468-53
; Sequence 53, Application PC/TUS9504468
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
; TITLE OF INVENTION: CIRCULARLY PERMUTATED FUSION PROTEINS
; NUMBER OF SEQUENCES: 59
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/04468
; FILING DATE: 07-APR-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/225,224
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Weber, Ellen L.
; REGISTRATION NUMBER: 32,762
; REFERENCE/DOCKET NUMBER: 15280-193-1PC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 6 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
PCT-US95-04468-53

Query Match 46.5%; Score 20; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 4.1e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 RPH 7
Db 1 RPH 3

RESULT 15
US-08-074-210-3
; Sequence 3, Application US/08074210
; Patent No. 5482930
; GENERAL INFORMATION:
; APPLICANT: Wei, Edward T.
; APPLICANT: Thomas, Holly A.
; TITLE OF INVENTION: ANTI-INFLAMMATORY COMPOSITION AND METHOD
; TITLE OF INVENTION: WITH DES-TYR DYNORPHIN AND ANALOGUES
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Majestic, Parsons, Siebert & Haue
; STREET: Four Embarcadero Center, Suite 1450
; CITY: San Francisco
```

; STATE: California  
; COUNTRY: U.S.A.  
; ZIP: 94111-4121  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/074,210  
; FILING DATE: 19930609  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Siebert, J. Suzanne  
; REGISTRATION NUMBER: 28,758  
; REFERENCE/DOCKET NUMBER: 2500.72  
; TELEPHONE: (415) 362-5556  
; TELEFAX: (415) 362-5418  
; TELEX: 278638 MGPS  
; INFORMATION FOR SEQ ID NO: 3:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 7 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; ANTI-SENSE: NO  
; US-08-074-210-3

Query Match 46.5%; Score 20; DB 1; Length 7;  
Best Local Similarity 75.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 3 RVRP 6  
Db 2 RIRP 5

Search completed: August 3, 2005, 11:58:10  
Job time : 27 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:57:01 ; Search time 89.3333 Seconds  
(without alignments)  
30.529 Million cell updates/sec

Title: US-09-910-582B-3  
Perfect score: 43  
Sequence: 1 HGRVRPH 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 71902

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Published Applications AA:\*

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- 22: /cgn2\_6/ptodata/2/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	43	100.0	7	10	US-09-910-582B-3
3	43	100.0	7	17	US-10-838-289-35
4	31	72.1	6	15	US-10-381-734-25
5	25	58.1	5	15	US-10-381-734-14
6	25	58.1	7	15	US-10-381-734-1
7	25	58.1	7	15	US-10-381-734-8
8	25	58.1	7	15	US-10-381-734-16
9	25	58.1	7	15	US-10-381-734-23
10	24	55.8	6	10	US-09-500-700-101
11	24	55.8	6	17	US-10-941-069-101
					Sequence 2, Appli
					Sequence 3, Appli
					Sequence 35, Appl
					Sequence 25, Appl
					Sequence 14, Appl
					Sequence 1, Appli
					Sequence 8, Appli
					Sequence 16, Appl
					Sequence 23, Appl
					Sequence 101, App
					Sequence 101, App

22	51.2	7	10	US-09-202-329-21	Sequence 21, Appl
21	48.8	4	18	US-10-892-402-102	Sequence 102, Appl
20	47.7	5	9	US-09-839-743-27	Sequence 27, Appl
20	46.5	7	16	US-10-363-204-55	Sequence 55, Appl
20	46.5	4	17	US-10-476-861A-10	Sequence 10, Appl
20	46.5	4	17	US-10-476-861A-52	Sequence 52, Appl
20	46.5	4	17	US-10-476-861A-127	Sequence 127, App
20	46.5	6	14	US-10-372-076-151	Sequence 151, App
20	46.5	6	16	US-10-677-074-151	Sequence 151, Appl
20	46.5	6	16	US-10-672-396-15	Sequence 15, Appl
20	46.5	7	9	US-09-803-951-3	Sequence 3, Appli
20	46.5	7	9	US-09-765-086-85	Sequence 85, Appl
20	46.5	7	10	US-09-978-309A-62	Sequence 62, Appl
20	46.5	7	11	US-09-855-604-23	Sequence 23, Appl
20	46.5	7	12	US-09-855-604-23	Sequence 23, Appl
20	46.5	7	14	US-10-264-374-85	Sequence 85, Appl
20	46.5	7	14	US-10-375-992-85	Sequence 85, Appl
20	46.5	7	15	US-10-264-374-85	Sequence 85, Appl
20	46.5	7	16	US-10-375-992-85	Sequence 85, Appl
20	46.5	7	17	US-10-838-289-646	Sequence 646, App
20	46.5	7	17	US-10-892-831-62	Sequence 62, Appl
20	46.5	7	17	US-10-892-831-62	Sequence 62, Appl
19	44.2	4	14	US-10-132-920B-52	Sequence 52, Appl
19	44.2	4	15	US-10-438-181A-52	Sequence 52, Appl
19	44.2	4	17	US-10-920-788-49	Sequence 49, Appl
19	44.2	5	15	US-10-436-549-174	Sequence 174, App
19	44.2	5	16	US-10-712-425-174	Sequence 174, App
19	44.2	5	17	US-10-773-032-174	Sequence 174, App
19	44.2	6	8	US-08-865-579-29	Sequence 29, Appl
19	44.2	6	9	US-09-746-731-29	Sequence 29, Appl
19	44.2	6	9	US-09-952-768-18	Sequence 18, Appl
19	44.2	6	9	US-09-954-697-67	Sequence 67, Appl
19	44.2	6	10	US-09-300-425B-34	Sequence 34, Appl
19	44.2	6	13	US-10-156-820-44	Sequence 44, Appl
19	44.2	6	13	US-10-059-749-29	Sequence 29, Appl
19	44.2	6	14	US-10-262-435-13	Sequence 13, Appl
19	44.2	6	14	US-10-086-208-13	Sequence 13, Appl
19	44.2	6	15	US-10-668-955-18	Sequence 18, Appl
19	44.2	6	16	US-10-699-088-578	Sequence 578, App
19	44.2	6	16	US-10-699-113-578	Sequence 578, App
19	44.2	6	16	US-10-704-363-75	Sequence 75, Appl
19	44.2	6	17	US-10-884-830-430	Sequence 430, App
19	44.2	6	17	US-10-699-114-578	Sequence 578, App
19	44.2	6	17	US-10-806-924-541	Sequence 541, App
19	44.2	7	10	US-09-954-385-70	Sequence 70, Appl
19	44.2	7	14	US-10-286-457-7	Sequence 7, Appli
19	44.2	7	14	US-10-232-544-48	Sequence 48, Appl
19	44.2	7	16	US-10-727-335-10	Sequence 10, Appl
19	44.2	7	17	US-10-912-512-70	Sequence 70, Appl
19	44.2	7	17	US-10-235-043-70	Sequence 43, App
19	44.2	7	17	US-10-052-578-217	Sequence 217, App
18	41.9	6	15	US-10-414-524-46	Sequence 46, Appl
18	41.9	6	18	US-10-975-157-36	Sequence 36, Appl
18	41.9	7	10	US-09-954-385-408	Sequence 408, App
18	41.9	7	10	US-09-990-832C-44	Sequence 44, Appl
18	41.9	7	14	US-10-211-088-180	Sequence 180, App
18	41.9	7	14	US-10-052-578-217	Sequence 217, App
18	41.9	7	14	US-10-053-520-217	Sequence 217, App
18	41.9	7	15	US-10-258-146A-75	Sequence 215, App
18	41.9	7	15	US-10-328-953-220	Sequence 220, App
18	41.9	7	16	US-10-258-144-110	Sequence 110, App
18	41.9	7	16	US-10-727-335-37	Sequence 37, Appl
18	41.9	7	17	US-10-783-311-343	Sequence 343, App
18	41.9	7	17	US-10-912-512-408	Sequence 408, App
18	41.9	7	17	US-10-235-043-408	Sequence 408, App
18	41.9	7	18	US-10-975-157-35	Sequence 35, Appl
17	40.7	6	17	US-10-884-830-436	Sequence 436, App
17	40.7	7	14	US-10-052-578-276	Sequence 276, App
17	40.7	7	14	US-10-053-520-276	Sequence 276, App
17	40.7	7	14	US-10-053-498B-276	Sequence 276, App
17	40.7	7	15	US-10-258-146A-134	Sequence 134, App
17	40.7	7	15	US-10-328-953-279	Sequence 279, App
17	40.7	7	16	US-10-258-144-169	Sequence 169, App

85 17 39.5 4 18 US-10-892-402-1114 Sequence 114, App  
86 17 39.5 6 9 US-09-904-599A-3 Sequence 3, Appl  
87 17 39.5 6 9 US-09-847-101B-46 Sequence 46, Appl  
88 17 39.5 6 13 US-10-156-820-75 Sequence 75, Appl  
89 17 39.5 6 15 US-10-414-523-12 Sequence 12, Appl  
90 17 39.5 6 15 US-10-297-229-13 Sequence 13, Appl  
91 17 39.5 6 16 US-10-699-088-580 Sequence 580, App  
92 17 39.5 6 16 US-10-699-088-758 Sequence 758, App  
93 17 39.5 6 16 US-10-699-088-759 Sequence 759, App  
94 17 39.5 6 16 US-10-699-088-1057 Sequence 1057, App  
95 17 39.5 6 16 US-10-699-088-1058 Sequence 1058, App  
96 17 39.5 6 16 US-10-699-113-146 Sequence 146, App  
97 17 39.5 6 16 US-10-699-113-147 Sequence 147, App  
98 17 39.5 6 16 US-10-699-113-580 Sequence 580, App  
99 17 39.5 6 16 US-10-699-113-758 Sequence 758, App  
100 17 39.5 6 16 US-10-699-113-759 Sequence 759, App

## ALIGNMENTS

RESULT 1  
US-09-782-650-2  
; Sequence 2, Application US/09782650  
; Patent No. US2002001950A1  
; GENERAL INFORMATION:  
; APPLICANT: Levine, Arnold J.  
; APPLICANT: Mitterer, Artur  
; APPLICANT: Falkner, Falko-Guenter  
; APPLICANT: Scheiflinger, Friedrich  
; APPLICANT: Dornier, Friedrich  
; APPLICANT: Edwards LifeSciences Corporation  
; TITLE OF INVENTION: Targeted Angiogenesis  
; FILE REFERENCE: 2053D-000611US  
; CURRENT APPLICATION NUMBER: US/09782, 650  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: US 09/324, 079  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: US 09/327, 045  
; PRIOR FILING DATE: 1999-06-07  
; PRIOR APPLICATION NUMBER: PCT/US00/14988  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: Patentin Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:targeting  
US-09-782-650-2

Query Match 100.0%; Score 43; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7  
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|  
Db 1 HGRVRPH 7

RESULT 2  
US-09-910-582B-3  
; Sequence 3, Application US/09910582B  
; Publication No. US20030045476A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Mackenna, Deirdre A.  
; TITLE OF INVENTION: Heart Homing Conjugates  
; FILE REFERENCE: P-LJ 4857  
; CURRENT APPLICATION NUMBER: US/09/910, 582B  
; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/326, 718  
; PRIOR FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-910-582B-3

Query Match 100.0%; Score 43; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7  
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|  
Db 1 HGRVRPH 7

RESULT 3  
US-10-838-289-35  
; Sequence 35, Application US/10838289  
; Publication No. US20050058603A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Jimming  
; APPLICANT: Ai, Hua  
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
; TITLE OF INVENTION: NANOSHELLS  
; FILE REFERENCE: CWRU-P01-040  
; CURRENT APPLICATION NUMBER: US/10/838, 289  
; CURRENT FILING DATE: 2004-05-03  
; PRIOR APPLICATION NUMBER: US 60/502, 429  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: US 60/467, 389  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 756  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 35  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Heart homing peptide  
US-10-838-289-35

Query Match 100.0%; Score 43; DB 17; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 HGRVRPH 7  
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|  
|  
Db 1 HGRVRPH 7

RESULT 4  
US-10-381-734-25  
; Sequence 25, Application US/10381734  
; Publication No. US20040092434A1  
; GENERAL INFORMATION:  
; APPLICANT: BETZ, NATACHA  
; APPLICANT: BIKFALVI, ANDREAS  
; APPLICANT: DELERIS, GERARD  
; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN  
; TITLE OF INVENTION: OR ACTIVATORS OF ANGIOGENESIS  
; FILE REFERENCE: 235834US0XPCT  
; CURRENT APPLICATION NUMBER: US/10/381, 734  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: PCT/FR01/03049  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: FR 00 012654  
; PRIOR FILING DATE: 2000-10-04

; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 25  
; LENGTH: 6  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Cyclic Peptide  
US-10-381-734-25

Query Match 72.1%; Score 31; DB 15; Length 6;  
Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 GVRVPH 7  
|:|:  
Db 1 GRIKPH 6

RESULT 5  
US-10-381-734-14  
; Sequence 14, Application US/10381734  
; Publication No. US20040092434A1  
; GENERAL INFORMATION:  
; APPLICANT: BETZ, NATACHA  
; APPLICANT: BIKFALVI, ANDREAS  
; APPLICANT: DELERIS, GERARD  
; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN  
; TITLE OF INVENTION: OR ACTIVATORS OF ANGIOGENESIS  
; FILE REFERENCE: 235834USXPCT  
; CURRENT APPLICATION NUMBER: US/10/381,734  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: PCT/FR01/03049  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: FR 00 012654  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 14  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-381-734-14

Query Match 58.1%; Score 25; DB 15; Length 5;  
Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7  
|:|:  
Db 1 RIKPH 5

RESULT 6  
US-10-381-734-1  
; Sequence 1, Application US/10381734  
; Publication No. US20040092434A1  
; GENERAL INFORMATION:  
; APPLICANT: BETZ, NATACHA  
; APPLICANT: BIKFALVI, ANDREAS  
; APPLICANT: DELERIS, GERARD  
; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN  
; TITLE OF INVENTION: OR ACTIVATORS OF ANGIOGENESIS  
; FILE REFERENCE: 235834USXPCT  
; CURRENT APPLICATION NUMBER: US/10/381,734  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: PCT/FR01/03049  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: FR 00 012654  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 25

; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Peptide  
US-10-381-734-1

Query Match 58.1%; Score 25; DB 15; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7  
|:|:  
Db 1 RIKPH 5

RESULT 7  
US-10-381-734-8  
; Sequence 8, Application US/10381734  
; Publication No. US20040092434A1  
; GENERAL INFORMATION:  
; APPLICANT: BETZ, NATACHA  
; APPLICANT: BIKFALVI, ANDREAS  
; APPLICANT: DELERIS, GERARD  
; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN  
; TITLE OF INVENTION: OR ACTIVATORS OF ANGIOGENESIS  
; FILE REFERENCE: 235834USXPCT  
; CURRENT APPLICATION NUMBER: US/10/381,734  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: PCT/FR01/03049  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: FR 00 012654  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 8  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial sequence  
; FEATURE:  
; OTHER INFORMATION: Synthetic Cyclic Peptide  
US-10-381-734-8

Query Match 58.1%; Score 25; DB 15; Length 7;  
Best Local Similarity 60.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRPH 7  
|:|:  
Db 1 RIKPH 5

RESULT 8  
US-10-381-734-16  
; Sequence 16, Application US/10381734  
; Publication No. US20040092434A1  
; GENERAL INFORMATION:  
; APPLICANT: BETZ, NATACHA  
; APPLICANT: BIKFALVI, ANDREAS  
; APPLICANT: DELERIS, GERARD  
; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN  
; TITLE OF INVENTION: OR ACTIVATORS OF ANGIOGENESIS  
; FILE REFERENCE: 235834USXPCT  
; CURRENT APPLICATION NUMBER: US/10/381,734  
; CURRENT FILING DATE: 2003-10-21  
; PRIOR APPLICATION NUMBER: PCT/FR01/03049  
; PRIOR FILING DATE: 2001-10-02  
; PRIOR APPLICATION NUMBER: FR 00 012654  
; PRIOR FILING DATE: 2000-10-04  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: PatentIn version 3.1

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; SEQ ID NO 16
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
US-10-381-734-16

Query Match          58.1%; Score 25; DB 15; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 RVRPH 7
      |.:||
Db      1 RIKPH 5

RESULT 9
US-10-381-734-23
; Sequence 23, Application US/10381734
; Publication No. US20040092434A1
; GENERAL INFORMATION:
; APPLICANT: BETZ, NATACHA
; APPLICANT: BIKFALVI, ANDREAS
; APPLICANT: DELERIS, GERARD
; TITLE OF INVENTION: CYCLOPEPTIDES, A METHOD FOR THEIR PREPARATION AND THEIR USE AS IN
; TITLE OF INVENTION: OR ACTIVATORS OF ANGIOGENESIS
; FILE REFERENCE: 235834USOXPC
; CURRENT APPLICATION NUMBER: US/10/381,734
; CURRENT FILING DATE: 2003-10-21
; PRIOR APPLICATION NUMBER: PCT/FR01/03049
; PRIOR FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: FR 00 012654
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Cyclic Peptide
; NAME/KEY: MOD RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: (D) Phe
US-10-381-734-23

Query Match          58.1%; Score 25; DB 15; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 RVRPH 7
      |.:||
Db      2 RIKPH 6

RESULT 10
US-09-500-700-101
; Sequence 101, Application US/09500700
; Publication No. US20030059767A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIPT160-4
; CURRENT APPLICATION NUMBER: US/09/500,700
; CURRENT FILING DATE: 2003-01-10
; PRIOR APPLICATION NUMBER: US 08/863,813
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: US 08/676,318
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; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCT/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119
; PRIOR FILING DATE: 1994-01-18
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified sequence of finger 2 of zif268
US-09-500-700-101

Query Match          55.8%; Score 24; DB 10; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VRPH 7
      ||||
Db      1 VRPH 4

RESULT 11
US-10-941-069-101
; Sequence 101, Application US/10941069
; Publication No. US20050084885A1
; GENERAL INFORMATION:
; APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
; APPLICANT: BARBAS III, Carlos F.
; APPLICANT: GOTTESFELD, Joel M.
; APPLICANT: WRIGHT, Peter E.
; TITLE OF INVENTION: ZINC FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
; FILE REFERENCE: SCRIPT160-4
; CURRENT APPLICATION NUMBER: US/10/941,069
; CURRENT FILING DATE: 2004-09-14
; PRIOR APPLICATION NUMBER: US/09/500,700
; PRIOR FILING DATE: 2000-02-09
; PRIOR APPLICATION NUMBER: US 08/863,813
; PRIOR FILING DATE: 1997-05-27
; PRIOR APPLICATION NUMBER: US 08/676,318
; PRIOR FILING DATE: 1996-12-30
; PRIOR APPLICATION NUMBER: PCT/US95/00829
; PRIOR FILING DATE: 1995-01-18
; PRIOR APPLICATION NUMBER: US 08/312,604
; PRIOR FILING DATE: 1994-09-28
; PRIOR APPLICATION NUMBER: US 08/183,119
; NUMBER OF SEQ ID NOS: 127
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 101
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Modified sequence of finger 2 of zif268
US-10-941-069-101

Query Match          55.8%; Score 24; DB 17; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      4 VRPH 7
      ||||
Db      1 VRPH 4

RESULT 12
US-09-202-329-21
; Sequence 21, Application US/09202329A
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Publication No. US20030124137A1  
; GENERAL INFORMATION:  
; APPLICANT: Dalton, John P  
; TITLE OF INVENTION: Vaccine containing a peroxiredoxin and/or a B-tubulin  
; FILE REFERENCE: 1181-243  
; CURRENT APPLICATION NUMBER: US/09/202,329A  
; PRIOR FILING DATE: 1999-02-19  
; EARLIER APPLICATION NUMBER: GB 9612214.8  
; EARLIER FILING DATE: 1996-06-11  
; EARLIER APPLICATION NUMBER: PCT/GB97/01573  
; EARLIER FILING DATE: 1997-06-11  
; NUMBER OF SEQ ID NOS: 21  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 21  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Fasciola hepatica  
US-09-202-329-21

Query Match 51.2%; Score 22; DB 10; Length 7;  
Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 HGRVRP 6  
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Db 1 HGEVCP 6

RESULT 13  
US-10-892-402-102  
; Sequence 102, Application US/10892402  
; Publication No. US20050153306A1  
; GENERAL INFORMATION:  
; APPLICANT: Harris, Jennifer L.  
; APPLICANT: Damoiseaux, Robert  
; APPLICANT: Backes, Bradley J.  
; APPLICANT: Winessinger, Nicolas  
; APPLICANT: IRM LLC  
; TITLE OF INVENTION: Fluorogenic Enzyme Substrates and Uses  
; TITLE OF INVENTION: Thereof  
; FILE REFERENCE: 021288-000410US  
; CURRENT APPLICATION NUMBER: US/10/892,402  
; CURRENT FILING DATE: 2004-07-14  
; PRIOR APPLICATION NUMBER: US 60/487,464  
; PRIOR FILING DATE: 2003-07-14  
; NUMBER OF SEQ ID NOS: 155  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 102  
; LENGTH: 4  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: rhodamine protease substrate library peptide  
US-10-892-402-102

Query Match 48.8%; Score 21; DB 18; Length 4;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 RVRP 6  
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Db 1 RVRP 4

RESULT 14  
US-09-839-743-27  
; Sequence 27, Application US/09839743  
; Patent No. US20020146824A1  
; GENERAL INFORMATION:  
; APPLICANT: The Salk Institute for Biological Sciences  
; APPLICANT: Lamb, Christopher  
; APPLICANT: Doerner, Peter

APPLICANT: Laible, Goetz  
; TITLE OF INVENTION: No. US20020146824A1el Transcription Enhancer Element and  
; FILE REFERENCE: SALKINS 008DV3  
; CURRENT APPLICATION NUMBER: US/09/839,743  
; CURRENT FILING DATE: 2001-04-19  
; PRIOR APPLICATION NUMBER: US 09/401,336  
; PRIOR FILING DATE: 1999-09-21  
; PRIOR APPLICATION NUMBER: US 09/189,344  
; PRIOR FILING DATE: 1998-11-10  
; PRIOR APPLICATION NUMBER: US 08/669,721  
; PRIOR FILING DATE: 1996-06-27  
; NUMBER OF SEQ ID NOS: 28  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 27  
; LENGTH: 5  
; TYPE: PRT  
; ORGANISM: Nicotiana tabacum  
US-09-839-743-27

Query Match 48.8%; Score 21; DB 9; Length 5;  
Best Local Similarity 80.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 GRVRP 6  
|||  
Db 1 GRPRP 5

RESULT 15  
US-10-363-204-55  
; Sequence 55, Application US/10363204  
; Publication No. US20040170955A1  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display  
; FILE REFERENCE: 005774.P003PCT  
; CURRENT APPLICATION NUMBER: US/10/363,204  
; CURRENT FILING DATE: 2003-03-07  
; NUMBER OF SEQ ID NOS: 251  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 55  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(7)  
; OTHER INFORMATION: synthetic construct  
US-10-363-204-55

Query Match 47.7%; Score 20.5; DB 16; Length 7;  
Best Local Similarity 71.4%; Pred. No. 1.6e+06;  
Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 1 HGR-VRP 6  
|||  
Db 1 HGOVRP 7

Search completed: August 3, 2005, 12:14:01  
Job time : 91.3333 secs

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## ALIGNMENTS

RESULT 1  
B44817  
34.5K structural protein - Leuconostoc oenos phase P2t11-15 (fragment)  
C;Species: Leuconostoc oenos phase P2t11-15  
C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C;Accession: B44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A;Title: Lysozyme in Leuconostoc oenos.  
A;Reference number: A44817; MUID:92085033; PMID:1748868  
A;Accession: B44817  
A;Molecule type: protein  
A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70342)

Query Match 58.6%; Score 17; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVTSS 7  
: |||  
Db 1 LATSS 5

RESULT 2  
D44817  
35K structural protein - Leuconostoc oenos phase PAT5-12 (fragment)  
C;Species: Leuconostoc oenos phase PAT5-12  
C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C;Accession: D44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A;Title: Lysozyme in Leuconostoc oenos.  
A;Reference number: A44817; MUID:92085033; PMID:1748868  
A;Accession: D44817  
A;Molecule type: protein  
A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70340)

Query Match 58.6%; Score 17; DB 2; Length 5;  
Best Local Similarity 80.0%; Pred. No. 2.8e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVTSS 7  
: |||  
Db 1 LATSS 5

RESULT 3  
H44817  
34.5K structural protein - Leuconostoc oenos phase P32 (fragment)  
C;Species: Leuconostoc oenos phase P32  
C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C;Accession: H44817

R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A;Title: Lysozyme in Leuconostoc oenos.  
A;Reference number: A44817; MUID:92085033; PMID:1748868  
A;Accession: H44817  
A;Molecule type: protein  
A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70332)

Query Match 51.7%; Score 15; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVTSS 7  
: |||  
Db 1 MATSS 5

RESULT 4  
F44817  
34.5K structural protein - Leuconostoc oenos phase P54 (fragment)  
C;Species: Leuconostoc oenos phase P54  
C;Date: 31-Mar-1993 #sequence\_revision 22-May-1998 #text\_change 22-May-1998  
C;Accession: F44817  
R;Arendt, E.K.; Lonvaud, A.; Hammes, W.P.  
J. Gen. Microbiol. 137, 2135-2139, 1991  
A;Title: Lysozyme in Leuconostoc oenos.  
A;Reference number: A44817; MUID:92085033; PMID:1748868  
A;Accession: F44817  
A;Molecule type: protein  
A;Residues: 1-5 <ARE>

A;Note: sequence extracted from NCBI backbone (NCBIP:70335)

Query Match 51.7%; Score 15; DB 2; Length 5;  
Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 LVTSS 7  
: |||  
Db 1 MATSS 5

RESULT 5  
B43848  
cell surface adhesin for heparan sulfate, 60K - Staphylococcus aureus (fragment)  
C;Species: Staphylococcus aureus  
C;Date: 10-Mar-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Feb-1995  
C;Accession: B43848  
R;Liang, O.D.; Ascencio, F.; Fransson, L.A.; Wadstrom, T.  
Infect. Immun. 60, 899-906, 1992  
A;Title: Binding of heparan sulfate to Staphylococcus aureus.  
A;Reference number: A43848; MUID:92176005; PMID:1541563  
A;Accession: B43848  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-4 <LIA>

A;Note: sequence extracted from NCBI backbone (NCBIP:85444)

Query Match 48.3%; Score 14; DB 2; Length 4;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLVT 5  
: |||  
Db 1 MLVT 4

RESULT 6  
E30608  
IG kappa chain V-III region (Gag) - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 29-Jun-1989 #sequence\_revision 29-Jun-1989 #text\_change 16-Aug-1996  
C;Accession: E30608  
R;Goni, F.R.; Chen, P.P.; McGinnis, D.; Arjonilla, M.L.; Fernandez, J.; Carson, D.; Solon  
J. Immunol. 142, 3158-3163, 1989  
A;Title: Structural and idiotypic characterization of the L chains of human IgM autoantibodies.  
A;Reference number: A30601; MUID:89215279; PMID:2496160  
A;Accession: E30608  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <GON>

C;Keywords: heterotetramer; immunoglobulin

Query Match 48.3%; Score 14; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 VVLVTS 6  
: |||

Db 2 IVLTQS 7

RESULT 7  
A30812  
sex pheromone ccf10 - Enterococcus faecalis  
C;Species: Enterococcus faecalis  
C;Date: 28-Feb-1990 #sequence\_revision 28-Feb-1990 #text\_change 09-Jul-2004  
C;Accession: A30812  
R;Mori, M.; Sakagami, Y.; Ishii, Y.; Isogai, A.; Kitada, C.; Fujino, M.; Adsit, J.C.; Du  
J. Biol. Chem. 263, 14574-14578, 1988  
A;Title: Structure of ccf10, a peptide sex pheromone which induces conjugative transfer  
A;Reference number: A30812; MUID:8908313; PMID:3139658  
A;Molecule type: protein  
A;Residues: 1-7 <MOR>  
A;Cross-references: UNIPROT:P20104

Query Match 44.8%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVT 5  
|||  
Db 1 LVT 3

RESULT 8  
A58725  
virotoxin - destroying angel  
C;Species: Amanita virosa (destroying angel)  
C;Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C;Accession: A58725  
R;Paulstich, H.; Buku, A.; Bodenmueller, H.; Wieland, T.  
Biochemistry 19, 334-343, 1980  
A;Title: Virotoxins: actin-binding cyclic peptides of Amanita virosa mushrooms.  
A;Reference number: A58725; MUID:6893271; PMID:6893271  
A;Accession: A58725  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <PAU>  
C;Keywords: D-amino acid; hydroxyproline; toxin; unencoded polypeptide  
F;1/7/Cross-link: cyclopeptide (Val-Leu) #status experimental  
F;2/Modified site: D-threonine (Thr) #status experimental  
F;3/Modified site: D-serine (Ser) #status experimental  
F;4/Modified site: (3R,4S)-3,4-dihydroxyproline (Pro) #status experimental  
F;6/Modified site: 2'-methylsulfonyltryptophan (Trp) #status experimental  
F;7/Modified site: 4,5-dihydroxyisoleucine (Leu) #status experimental

Query Match 44.8%; Score 13; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 VTS 6  
|||  
Db 1 VTS 3

RESULT 9  
I49808  
D-SP2.5 region - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 05-Nov-1999  
C;Accession: I49808  
R;Kurosawa, Y.; Tonegawa, S.  
J. Exp. Med. 155, 201-218, 1982  
A;Title: Organization, structure, and assembly of immunoglobulin heavy chain diversity D  
A;Reference number: I49808; MUID:82099936; PMID:6798155  
A;Accession: I49808  
A;Status: preliminary; translated from GB/EMBL/DBD  
A;Molecule type: DNA  
A;Residues: 1-6 <RES>  
A;Cross-references: GB:J00432; NID:G194370; PIDN:AAA37904.1; PID:G450452

C;Genetics:  
A;Gene: Igh

Query Match 41.4%; Score 12; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTS 6  
|||  
Db 3 MVTT 6

RESULT 10  
S70335  
endosperm protein, 40K - rye (fragment)  
C;Species: Secale cereale (rye)  
C;Date: 19-Mar-1998 #sequence\_revision 17-Apr-1998 #text\_change 17-Apr-1998  
C;Accession: S70335  
R;Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.  
Biochim. Biophys. Acta 1295, 13-22, 1996  
A;Title: Identification of major rye secalins as coeliac immunoreactive proteins.  
A;Reference number: S70327; MUID:96283789; PMID:8679669  
A;Accession: S70335  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <ROC>

Query Match 37.9%; Score 11; DB 2; Length 7;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVL 3  
|||  
Db 1 IVL 3

RESULT 11  
A27897  
glucan 1,4-alpha-glucosidase (EC 3.2.1.3) - Aspergillus phoenicis (fragment)  
N;Alternate names: glucoamylase  
C;Species: Aspergillus phoenicis  
C;Date: 16-Aug-1988 #sequence\_revision 16-Aug-1988 #text\_change 06-Dec-1996  
C;Accession: A27897  
R;Inokuchi, N.; Takahashi, T.; Irie, M.  
J. Biochem. 90, 1055-1067, 1981  
A;Title: Purification and characterization of a minor glucoamylase from Aspergillus saitoi  
A;Reference number: A27897; MUID:82075730; PMID:6796572  
A;Note: Aspergillus saitoi  
A;Accession: A27897  
A;Molecule type: protein  
A;Residues: 1-4 <INO>  
C;Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 34.5%; Score 10; DB 2; Length 4;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLV 4  
|||  
Db 2 VIV 4

RESULT 12  
A40135  
branched-chain-amino-acid transaminase (EC 2.6.1.42), mitochondrial - rat (fragment)  
N;Alternate names: branched-chain-amino-acid aminotransferase, mitochondrial  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 13-May-1992 #sequence\_revision 13-May-1992 #text\_change 30-Sep-1993  
C;Accession: A40135  
R;Hutson, S.M.; Wallin, R.; Hall, T.R.  
submitted to the Protein Sequence Database, March 1992  
A;Reference number: A40135  
A;Accession: A40135

A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-4 <HUT>  
C;Keywords: aminotransferase; mitochondrion

Query Match 34.5%; Score 10; DB 2; Length 4;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VTSS 7  
|:|:  
Db 1 VSSN 4

## RESULT 13

B31836  
20K protein - Rickettsia rickettsii (fragment)  
C;Species: Rickettsia rickettsii  
C;Date: 31-Mar-1990 #sequence\_revision 31-Mar-1990 #text\_change 28-May-1999  
C;Accession: B31836  
R;Anderson, B.E.; Baumstark, B.R.; Bellini, W.J.  
J. Bacteriol. 170, 4493-4500, 1988  
A;Title: Expression of the gene encoding the 17-kilodalton antigen from Rickettsia rickettsii  
A;Reference number: A91885; MUID:89008059; PMID:3139629  
A;Accession: B31836  
A;Molecule type: DNA  
A;Residues: 1-5 <AND>  
A;Cross-references: GB:J03371; NID:G152455; PIDN:AA15030.1; PID:G4262874

Query Match 34.5%; Score 10; DB 2; Length 5;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 TSS 7  
|:|:  
Db 3 TNS 5

## RESULT 14

E42364  
flagellar protein flhR - Salmonella typhimurium (fragment)  
C;Species: Salmonella typhimurium  
C;Date: 24-Jul-1992 #sequence\_revision 24-Jul-1992 #text\_change 09-Jul-2004  
C;Accession: E42364  
R;Vogler, A.P.; Homma, M.; Irikura, V.M.; Macnab, R.M.  
J. Bacteriol. 173, 3564-3572, 1991  
A;Title: Salmonella typhimurium mutants defective in flagellar filament regrowth and secretion  
A;Reference number: A42364; MUID:91258342; PMID:1646201  
A;Accession: E42364  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-5 <VOG>  
A;Cross-references: UNIPROT:P26416; GB:M62408

Query Match 34.5%; Score 10; DB 2; Length 5;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 LVT 5  
|:|:  
Db 1 MIT 3

## RESULT 15

PQ0728  
unidentified 5.0/16K protein [imported] - rice (fragment)  
C;Species: Oryza sativa (rice)  
C;Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 20-Apr-2000  
C;Accession: PQ0728  
R;Komatsu, S.; Kajiwara, H.; Hirano, H.  
Theor. Appl. Genet. 86, 935-942, 1993  
A;Title: A rice protein library; a data-file of rice proteins separated by two-dimensional gel electrophoresis  
A;Reference number: PQ0696

A;Accession: PQ0728  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-7 <KON>

Query Match 34.5%; Score 10; DB 2; Length 7;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 VVLV 4  
|:|:  
Db 3 IXLV 6

Search completed: August 3, 2005, 11:42:32  
Job time : 19 secs

GenCore version 5.1.6  
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# OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 88.6667 Seconds  
(without alignments)  
40.427 Million cell updates/sec

Title: US-09-910-582B-4

Perfect score: 29

Sequence: 1 VVLVTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 174

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Uniprot 03:\*

1: uniprot\_sprot:\*

2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	13	44.8	7	1	CCFL_ENTFA
2	13	44.8	7	2	P70804
3	13	44.8	7	2	P72081
4	12	41.4	7	2	Q54248
5	11	37.9	7	2	O42564
6	10	34.5	7	1	CIA_ENTFA
7	10	34.5	7	1	GFRP_MOUSE
8	9	31.0	4	1	YLM1_YEAST
9	9	31.0	7	1	IGAO_DACDE
10	9	31.0	7	2	P83492
11	9	31.0	7	2	P82445
12	9	31.0	7	2	Q9C5B3
13	9	31.0	7	2	P83530
14	8	27.6	4	1	ILME_SEPOF
15	8	27.6	4	2	Q08433
16	8	27.6	5	1	BI0B_CITFR
17	8	27.6	5	1	E104_LITRU
18	8	27.6	6	1	ACPH_RABIT
19	8	27.6	6	1	LOK1_LOCOMI
20	8	27.6	6	2	P82541
21	8	27.6	7	2	P93233
22	8	27.6	7	2	O07354
23	8	27.6	7	2	Q47029
24	8	27.6	7	2	Q65578
25	8	27.6	7	2	Q8JES1
26	7	24.1	5	1	BIOA_CITFR
27	7	24.1	5	1	PRCT_CARMA
28	7	24.1	5	1	PRCT_LIMPO
29	7	24.1	5	1	PRCT_PERAM
30	7	24.1	7	2	Q15897
31	7	24.1	7	2	O99182

32	6	20.7	4	1	EOSI_HUMAN
33	6	20.7	5	1	PSK_DAUCA
34	6	20.7	6	1	TMOF_SARBU
35	6	20.7	6	1	UN06_CLOPA
36	6	20.7	6	1	VP19_HHV1K
37	6	20.7	6	2	P83533
38	6	20.7	7	1	UC24_MAIZE
39	6	20.7	7	2	Q8MFY6
40	6	20.7	7	2	O34028
41	6	20.7	7	2	Q8KMS3
42	6	20.7	7	2	Q47505
43	6	20.7	7	2	Q8GL00
44	6	20.7	7	2	Q8GL04
45	6	20.7	7	2	Q66205
46	5	17.2	4	1	TUFT_HUMAN
47	5	17.2	5	1	AP21_EISFO
48	5	17.2	5	1	RE31_LITRU
49	5	17.2	5	1	RE32_LITRU
50	5	17.2	5	2	P83073
51	5	17.2	6	1	CIP1_MYTED
52	5	17.2	6	1	CIP2_MYTED
53	5	17.2	6	2	P82181
54	5	17.2	6	2	P82182
55	5	17.2	7	1	CARP_MYTED
56	5	17.2	7	1	FAR3_HAECO
57	5	17.2	7	1	FAR3_PANRE
58	5	17.2	7	1	PPH2_LYCES
59	5	17.2	7	1	UHL1_RAT
60	5	17.2	7	2	Q8TA04
61	5	17.2	7	2	Q8GL12
62	5	17.2	7	2	Q67113
63	5	17.2	7	2	Q9YQ10
64	4	13.8	4	1	FAR3_HIRME
65	4	13.8	4	1	FLRF_HIRME
66	4	13.8	4	1	FLRN_ATEL
67	4	13.8	4	1	OCP3_OCTMI
68	4	13.8	5	1	AL14_CARMA
69	4	13.8	5	1	E103_LITRU
70	4	13.8	5	1	FAR3_CHICK
71	4	13.8	5	1	MPA4_JUNVI
72	4	13.8	5	1	RE11_LITRU
73	4	13.8	5	1	TPIS_CANFA
74	4	13.8	5	1	UC22_MAIZE
75	4	13.8	5	1	UXA4_CHLTR
76	4	13.8	6	1	E101_LITRU
77	4	13.8	6	1	SAPP_SEPOF
78	4	13.8	6	1	TRP1_PSEPU
79	4	13.8	7	1	ALL2_CARMA
80	4	13.8	7	1	ALL3_CARMA
81	4	13.8	7	1	ALL4_CARMA
82	4	13.8	7	1	ALL5_CARMA
83	4	13.8	7	1	ALL7_CVDPO
84	4	13.8	7	1	CHOX_ALCSP
85	4	13.8	7	1	FAF2_ASCSU
86	4	13.8	7	1	FAF2_PANRE
87	4	13.8	7	1	FAR1_HELTI
88	4	13.8	7	1	FAR1_MACRS
89	4	13.8	7	1	FAR1_PROCL
90	4	13.8	7	1	FAR2_PROCL
91	4	13.8	7	1	HY7_PIG
92	4	13.8	7	1	LANC_CARUI
93	4	13.8	7	1	MNPI_LEPDE
94	4	13.8	7	1	TPFY_PACDA
95	4	13.8	7	1	UF03_MOUSE
96	4	13.8	7	1	UN06_PINPS
97	4	13.8	7	1	WWA1_ACHFU
98	4	13.8	7	1	WWA2_ACHFU
99	4	13.8	7	1	WWA3_ACHFU
100	4	13.8	7	2	Q8NH7

ALIGNMENTS

RESULT 1  
CCFL\_ENTFA STANDARD; PRT; 7 AA.  
ID P20104;  
AC 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)  
DE 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Sex pheromone cCF10;  
OS Enterococcus faecalis (Streptococcus faecalis).  
OC Bacteria; Firmicutes; Lactobacillales; Enterococcaceae; Enterococcus.  
OX NCBI\_TaxID=1351;  
RN [1]  
RP SEQUENCE  
RX MEDLINE=89008313; PubMed=3139658;  
RA Mori M., Sakagami Y., Ishii Y., Isogai A., Kitada C., Fujino M.,  
RA Adait J.C., Dunny G.M., Suzuki A.;  
RT "Structure of cCF10, a peptide sex pheromone which induces conjugative  
RT transfer of the Streptococcus faecalis tetracycline resistance  
RT plasmid, pCF10.";  
RL J. Biol. Chem. 263:14574-14578(1988).  
CC -!- FUNCTION: cCF10 is involved in the conjugative transfer of the  
CC hemolysin plasmid pCF10.  
DR PIR; A30812; A30812.  
KW Direct protein sequencing; Pheromone.  
SQ SEQUENCE 7 AA; 790 MW; 72C9D2C731B2C740 CRC64;  
Query Match 44.8%; Score 13; DB 1; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3 LVT 5  
Db 1 LVT 3

RESULT 2  
P70804 PRELIMINARY; PRT; 7 AA.  
ID P70804;  
AC 01-FEB-1997 (TReMBLrel. 02, Created)  
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
DE Algt protein (fragment).  
DE Name=algt;  
OS Azotobacter vinelandii.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Azotobacter.  
OX NCBI\_TaxID=354;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=E;  
RX MEDLINE=96427318; PubMed=8830682;  
RA Rehm B.H.A., Estesvag H., Valla S.;  
RT "A new Azotobacter vinelandii mannuronan C-5-epimerase gene (algG) is  
RT part of an alg gene cluster physically organized in a manner similar  
RT to that in Pseudomonas aeruginosa.";  
RL J. Bacteriol. 178:5884-5889(1996).  
DR EMBL; X87973; CAA61230.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 684 MW; 71B5A5A5A2D1AED0 CRC64;  
Query Match 44.8%; Score 13; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VTSS 7  
Db 3 VSSS 6

RESULT 3  
P72081 PRELIMINARY; PRT; 7 AA.  
ID P72081;  
AC 01-FEB-1997 (TReMBLrel. 02, Created)  
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)  
DE 3'-methylcephem hydroxylase (Fragment).  
DE Name=cefF;  
OS Nocardia lactamdurans.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Pseudonocardineae; Pseudonocardaceae; Amycolatopsis.  
OX NCBI\_TaxID=1913;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=96009872; PubMed=7557411; DOI=10.1016/0378-1119(95)00308-S;  
RA Coque J., Perez-Llarena F.J., Enguita F.J., Fuente J.L., Martin J.F.,  
RA Liras P.;  
RT "Characterization of the cmcH genes of Nocardia lactamdurans and  
RT Streptomyces clavuligerus encoding a functional 3'-hydroxymethylcephem  
RT O-carbamoyltransferase for cephamycin biosynthesis.";  
RL Gene 162:21-27(1995).  
DR EMBL; Z21682; CAA79797.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 746 MW; 75A1B2CDD1B681C0 CRC64;  
Query Match 44.8%; Score 13; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 4 VTS 6  
Db 5 VTS 7

RESULT 4  
Q54248 PRELIMINARY; PRT; 7 AA.  
ID Q54248;  
AC 01-NOV-1996 (TReMBLrel. 01, Created)  
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)  
DE RpLO protein (Fragment).  
DE Name=rplo;  
OS Streptomyces griseus.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1911;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=N2-3-11;  
RX MEDLINE=20011291; PubMed=10542330;  
RA Poehling S., Piepersberg W., Wehmeier U.F.;  
RT "Analysis and regulation of the sec Y gene from Streptomyces griseus  
RT N2-3-11 and interaction of the SecY protein with the SecA protein.";  
RL Biochim. Biophys. Acta 1447:298-302(1999).  
DR EMBL; X95915; CAA65160.1; -.  
FT NON\_TER 1  
SQ SEQUENCE 7 AA; 760 MW; 72C72B01B2D1B2A0 CRC64;  
Query Match 41.4%; Score 12; DB 2; Length 7;  
Best Local Similarity 75.0%; Pred. No. 1.6e+06;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
QY 2 VLVT 5  
Db 1 VTVT 4

RESULT 5  
O42564 PRELIMINARY; PRT; 7 AA.  
ID O42564;  
AC O42564;  
DT 01-JAN-1998 (TReMBLrel. 05, Created)  
DT 01-JAN-1998 (TReMBLrel. 05, Last sequence update)

DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	GTP cyclohydrolase I feedback regulatory protein (P35) (Fragment).
GN	Name=Gchfr; Synonyms=Gfrp;
OS	Mus musculus (Mouse).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX	NCBI_TaxID=10090;
ON	[1]
RN	SEQUENCE.
RC	TISSUE=Liver;
RA	Sanchez J.-C., Rouge V., Prutiger S., Hughes G., Van J.X.,
RA	Hoogland C., Appel R.D., Binz P.-A., Hochstrasser D.F., Cowthorne M.;
RL	Submitted (AUG-1998) to Swiss-Prot.
CC	-!- FUNCTION: Mediates tetrahydrobiopterin inhibition of GTP
CC	cyclohydrolase I. This inhibition is reversed by L-phenylalanine
CC	(By similarity).
CC	-!- SUBUNIT: Homodimer (By similarity).
DR	SWISS-2DPAGE; P99025; MOUSE.
KW	Direct protein sequencing.
FT	INIT MET 0 0
FT	NON TER 7 7
SQ	SEQUENCE 7 AA; 806 MW; 71B5B057273B4700 CRC64;
QY	2 VLVTS 6
DB	3 LLIST 7
RESULT 8	
YLMI YEAST	
ID	YLMI YEAST STANDARD; PRT; 4 AA.
AC	P36515;
DT	01-JUN-1994 (Rel. 29, Created)
DT	01-JUN-1994 (Rel. 29, Last sequence update)
DT	05-JUL-2004 (Rel. 44, Last annotation update)
DE	Mitochondrial 60S ribosomal protein L1 (Yml1) (Fragment).
GN	Name=YML1;
OS	Saccharomyces cerevisiae (Baker's yeast).
OC	Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC	Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX	NCBI_TaxID=4932;
ON	[1]
RN	SEQUENCE.
RA	MEDLINE=91285106; PubMed=2060626; DOI=10.1016/0014-5793(91)80759-V;
RA	Grohmann L., Graack H.-R., Kruff V., Choli T., Goldschmidt-Reisin S.;
RA	Kitakawa M.;
RT	"Extended N-terminal sequencing of proteins of the large ribosomal
RT	subunit from yeast mitochondria.";
RT	FEBS Lett. 284:51-56(1991).
CC	-!- FUNCTION: Putative component of the large subunit of mitochondrial
CC	ribosome.
CC	-!- SUBCELLULAR LOCATION: Mitochondrial.
DR	Pir; S17255; S17255.
KW	Direct protein sequencing; Mitochondrion; Ribosomal protein.
FT	NON TER 4 4
FT	NON TER 4 4
SQ	SEQUENCE 4 AA; 402 MW; 7771B2D5D0000000 CRC64;
QY	4 VT 5
DB	2 VT 3
RESULT 9	
IGAO DACDE	
ID	IGAO DACDE STANDARD; PRT; 7 AA.

AC P06294;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 05-JUN-2004 (Rel. 44, Last annotation update)  
 DE Galactose oxidase inhibitor.  
 OS Dactylium dendroides (Cladobotryum dendroides).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Hypocreaceae; Hypomyces.  
 OX NCBI\_TaxID=5132;  
 RN [1]  
 RP SEQUENCE.  
 RA Avigad G., Markus Z.;  
 RT "Identification of a peptide inhibitor of galactose oxidase from  
 Dactylium dendroides.", 1973.  
 RL Fed. Proc. 31:447-447(1973).  
 CC -1- FUNCTION: Binds one copper ion per molecule but does not bind the  
 CC galactose oxidase apoenzyme. It may inactivate the enzyme by  
 CC binding to its prosthetic copper group.  
 DR PIR: A01341; XEYDGD.  
 KW Copper; Direct protein sequencing; Metalloenzyme inhibitor.  
 SQ SEQUENCE 7 AA; 706 MW; 75BB01A456D87DB0 CRC64;  
 Query Match 31.0%; Score 9; DB 1; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 5 TSS 7  
 Db 5 TES 7

RESULT 10  
 P83492 ID P83492 PRELIMINARY; PRT; 7 AA.  
 AC P83492;  
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Alkaline protease Gr3 (EC 3.4.21.-) (Fragment).  
 OS Bionectria ochroleuca (Gliocladium roseum).  
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;  
 OC Hypocreomycetidae; Hypocreales; Bionectriaceae; Bionectria.  
 OX NCBI\_TaxID=29856;  
 RN [1]  
 RP SEQUENCE, FUNCTION, AND SUBCELLULAR LOCATION.  
 RC STRAIN=Gr87;  
 RA Zhao M., Zhang K.;  
 RL Submitted (DCC-2002) to Swiss-Prot.  
 CC -1- FUNCTION: Acts as a serine protease.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S8.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 DR GO; GO:0004252; F:serine-type endopeptidase activity; NAS.  
 DR InterPro; IPR00209; Pept\_S8\_S53.  
 DR PROSITE; PS00136; SUBTILASE\_ASP; PARTIAL.  
 DR PROSITE; PS00137; SUBTILASE\_HIS; PARTIAL.  
 DR PROSITE; PS00138; SUBTILASE\_SER; PARTIAL.  
 KW Hydrolase; Serine protease.  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 688 MW; 776DD455A6C1ADB0 CRC64;  
 Query Match 31.0%; Score 9; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 Qy 5 TSS 7  
 Db 2 TQS 4

RESULT 11  
 P82445 ID P82445 PRELIMINARY; PRT; 7 AA.  
 AC P82445;  
 DT 01-JUN-2000 (TrEMBLrel. 14, Created)  
 DT 01-JUN-2000 (TrEMBLrel. 14, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE 10 kDa cell wall protein (Fragment).  
 OS Nicotiana tabacum (Common tobacco).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC lamids; Solanales; Solanaceae; Nicotiana.  
 OX NCBI\_TaxID=4097;  
 RN [1]  
 RP SEQUENCE.  
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,  
 RA Wojtaszek P., Bolwell G.P.;  
 RT "Proteomic study of secondary cell wall proteins from transformed  
 RT tobacco culture.",  
 RL Planta 0:0-0(2000).  
 CC -1- SUBCELLULAR LOCATION: CELL WALL.  
 CC -1- TISSUE SPECIFICITY: XYLEM.  
 DR GO; GO:0005618; C:cell wall; IEA.  
 KW Cell wall.  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 758 MW; 69D2C1E862D1B2A0 CRC64;  
 Query Match 31.0%; Score 9; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 4 VT 5  
 Db 1 VT 2

RESULT 12  
 Q9C5B3 ID Q9C5B3 PRELIMINARY; PRT; 7 AA.  
 AC Q9C5B3;  
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)  
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Hypothetical protein DiDi 10A-2b (Fragment).  
 GN NamesDiDi 10A-2b;  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Roots;  
 RX MEDLINE=21171025; PubMed=1127426;  
 RA Vercauteren I., Van Der Schueren E., Van Montagu M., Gheysen G.;  
 RT "Arabidopsis thaliana genes expressed in the early compatible  
 RT interaction with root-knot nematodes.",  
 RL Mol. Plant Microbe Interact. 14:288-299(2001).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Roots;  
 RA Vercauteren I.J.R.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AJ286350; CAB71014.2; -.  
 KW Hypothetical protein.  
 FT NON TER 1  
 FT NON TER 7  
 FT NON TER 7  
 SQ SEQUENCE 7 AA; 719 MW; 6732C7287EB325D0 CRC64;  
 Query Match 31.0%; Score 9; DB 2; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VVL 3  
 Db 1 VT 3



Db 5 LVL 7

RESULT 13

P83530 PRELIMINARY; PRT; 7 AA.

AC P83530; 24, Created)

DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Unknown protein from 2D-page (Fragment).

OS Lactobacillus sanfranciscensis (Lactobacillus sanfrancisco).

OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;

OC Lactobacillus.

OX NCBI\_TaxID=1625;

RN [1]

RP SEQUENCE.

RC STRAIN=DSM 20451;

RX PubMed=12112860;

RX DOI=10.1002/1615-9861(200206)2:6<765::AID-PROT765>3.0.CO;2-V;

RA Drews O., Weiss W., Reil G., Parlar H., Wait R., Goerg A.;

RT "High pressure effects step-wise altered protein expression in

RT Lactobacillus sanfranciscensis.";

RL Proteomics 2:765-774(2002).

CC -!- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown

CC protein is: 15 kDa.

FT NON TER 1 1

FT NON TER 7 7

SQ SEQUENCE 7 AA; 790 MW; 6AAB02CAA731B2A0 CRC64;

Query Match 31.0%; Score 9; DB 2; Length 7;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VT 5

Db 1 VT 2

RESULT 14

ILME SEPOF STANDARD; PRT; 4 AA.

AC P83568;

DT 29-MAR-2004 (Rel. 43, Created)

DT 29-MAR-2004 (Rel. 43, Last sequence update)

DT 05-JUL-2004 (Rel. 44, Last annotation update)

DE Pheromone peptide ILME.

OS Sepia officinalis (Common cuttlefish).

OC Eukaryota; Metazoa; Mollusca; Cephalopoda; Coleoidea; Neocoleoidea;

OC Decapodiformes; Sepioidea; Sepiidae; Sepia.

OX NCBI\_TaxID=6610;

RN [1]

RP SEQUENCE, SUBCELLULAR LOCATION, TISSUE SPECIFICITY, AND MASS

RP SPECTROMETRY.

RC TISSUE=Egg;

RX MEDLINE=20403899; PubMed=10944467; DOI=10.1006/bbrc.2000.3286;

RA Zatylny C., Gagnon J., Boucaud-Camou E., Henry J.;

RT "ILME: a waterborne pheromonal peptide released by the eggs of Sepia

RT officinalis.";

RL Biochem. Biophys. Res. Commun. 275:217-222(2000).

RN [2]

RP SEQUENCE.

RC TISSUE=Egg;

RX MEDLINE=22197108; PubMed=12207899; DOI=10.1016/S0006-291X(02)02036-3;

RA Zatylny C., Marvin L., Gagnon J., Henry J.;

RT "Fertilization in Sepia officinalis: the first mollusk sperm-

RT attracting peptide.";

RL Biochem. Biophys. Res. Commun. 296:1186-1193(2002).

CC -!- FUNCTION: Has myotropic activity targeting the genital tract.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- TISSUE SPECIFICITY: Follicle, fully grown oocyte and egg(EC2).

CC -!- MASS SPECTROMETRY: MW=505.4; METHOD=MALDI; RANGE=1-4; NOTE=Ref.1.

KW Direct protein sequencing; Pheromone.

SQ SEQUENCE 4 AA; 505 MW; 6B169720300000000 CRC64;

Query Match 27.6%; Score 8; DB 1; Length 4;

Best Local Similarity 33.3%; Pred. No. 1.6e+06;

Matches 1; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 2 VLV 4

Db 1 ILM 3

RESULT 15

Q08433 PRELIMINARY; PRT; 4 AA.

AC Q08433;

DT 01-NOV-1996 (T-EMBLrel. 01, Created)

DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)

DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)

DE Bilirubin UDP-glucuronosyltransferase (Fragment).

OS Rattus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI\_TaxID=10118;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Gunn;

RX MEDLINE=91282758; PubMed=1840486;

RA Sato H., Aono S., Kashiwamata S., Koiwai O.;

RT "Genetic defect of bilirubin UDP-glucuronosyltransferase in the

RT hyperbilirubinemic Gunn rat.";

RL Biochem. Biophys. Res. Commun. 177:1161-1164(1991).

DR EMBL; S38636; AAB19259.1; -

DR GO; GO:0016740; F:transferase activity; IEA.

KW Transferase.

FT NON TER 4 4

SQ SEQUENCE 4 AA; 473 MW; 633732C4200000000 CRC64;

Query Match 27.6%; Score 8; DB 2; Length 4;

Best Local Similarity 100.0%; Pred. No. 1.6e+06;

Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VL 3

Db 2 VL 3

Search completed: August 3, 2005, 12:07:39

Job time : 88.6667 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:27 ; Search time 96.3333 Seconds  
(without alignments)  
28.104 Million cell updates/sec

Title: US-09-910-582B-4

Perfect score: 29

Sequence: 1 VVLVTSS 7

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 121728

Minimum DB seq length: 0

Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

- A\_Geneseq\_16Dec04:\*
- 1: Geneseq1980s:\*
  - 2: Geneseq1990s:\*
  - 3: Geneseq2000s:\*
  - 4: Geneseq2001s:\*
  - 5: Geneseq2002s:\*
  - 6: Geneseq2003as:\*
  - 7: Geneseq2003bs:\*
  - 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	7	4	AAB30897 Peptide w
2	29	100.0	7	4	AAB50799 Heart hom
3	19	65.5	6	2	AAB43141 Anti-meli
4	19	65.5	7	7	ADE39237 Oestrogen
5	18	62.1	5	7	ADC55448 Epimorphi
6	18	62.1	6	7	ADC55447 Epimorphi
7	18	62.1	7	3	AAV15720 Peptide u
8	18	62.1	7	3	AAV80874 Fluoropho
9	18	62.1	7	7	ADC55446 Epimorphi
10	17	58.6	4	2	AAR34100 Peptide w
11	17	58.6	4	2	AAR34038 Peptide w
12	17	58.6	4	2	AAR34090 Peptide w
13	17	58.6	5	3	AAB16520 Angiogene
14	17	58.6	5	5	AAW48891 Fibrinoge
15	17	58.6	5	7	ADD12160 Tumour su
16	17	58.6	6	2	AAR34098 Antigen t
17	17	58.6	6	2	AAR34036 Antigen t
18	17	58.6	6	2	AAR34088 Antigen t
19	17	58.6	6	2	AAW25205 VTL-Pepti
20	17	58.6	6	2	AAW43157 Anti-meli
21	17	58.6	6	5	ABG35151 Ovarian c
22	17	58.6	6	5	ABG60399 Selective
23	17	58.6	6	7	ADD12161 Tumour su
24	17	58.6	7	2	AAR44042 Agarase e
25	17	58.6	7	2	AAR8312 Beta-agar

26	17	58.6	7	2	AAW73145
27	17	58.6	7	5	ABG96763
28	17	58.6	7	7	ADD12162 Tumour su
29	17	58.6	7	7	ADL98580 Human leu
30	17	58.6	7	8	ADI38690 Cancer va
31	16	55.2	5	2	AAR12433
32	16	55.2	5	8	ADR28814
33	16	55.2	6	2	AAR05972 Somatic i
34	16	55.2	6	2	AAW43142 Anti-meli
35	16	55.2	6	2	AAW43135 Anti-meli
36	16	55.2	6	2	AAW43134 Anti-meli
37	16	55.2	6	4	AAB48417 Human ICA
38	16	55.2	6	5	ABG90504 Hominidae
39	16	55.2	6	7	ABM74170 DNA clone
40	16	55.2	7	2	AAR26350 Fungicida
41	16	55.2	7	2	AAR90626 S. solfat
42	16	55.2	7	2	AAW25759 PHA depol
43	16	55.2	7	2	AAW25759 Membrane
44	16	55.2	7	3	AAW76119 Rat nerve
45	16	55.2	7	3	AAW90823 Murine sk
46	16	55.2	7	4	AAB56058 Skin cell
47	16	55.2	7	4	AAB81547 Zif268 zi
48	16	55.2	7	5	ABB72258 Murine pe
49	16	55.2	7	6	ABP58769 Peptide c
50	16	55.2	7	7	ADA07589 Human sec
51	16	55.2	7	8	ADJ87953 Bioactive
52	16	55.2	7	8	ADN41515 Novel hum
53	15	51.7	5	5	ABBS9064 N-termina
54	15	51.7	5	5	AAU85442 Human col
55	15	51.7	5	6	ABP70390 Tryptic p
56	15	51.7	5	8	ADI00219 Endopin-2
57	15	51.7	5	8	ADI00220 Endopin-2
58	15	51.7	6	2	AAR57003 N-termina
59	15	51.7	6	2	AAR85518 Anti-meli
60	15	51.7	6	2	AAW08672 Honeybee
61	15	51.7	6	2	AAW08699 Honeybee
62	15	51.7	6	2	AAW43136 Anti-meli
63	15	51.7	6	2	AAW43138 Anti-meli
64	15	51.7	6	2	AAW43129 Anti-meli
65	15	51.7	6	2	AAW43140 Anti-meli
66	15	51.7	6	2	AAW43143 Anti-meli
67	15	51.7	6	2	AAW43130 Anti-meli
68	15	51.7	6	2	AAW43139 Anti-meli
69	15	51.7	6	2	AAW43144 Peptide #
70	15	51.7	6	2	AAW43131 Anti-meli
71	15	51.7	6	2	AAW43137 Anti-meli
72	15	51.7	6	2	AAW43132 Anti-meli
73	15	51.7	6	2	AAW43146 Peptide #
74	15	51.7	6	2	AAW43117 Anti-meli
75	15	51.7	6	2	AAW43147 Peptide #
76	15	51.7	6	2	AAW43133 Anti-meli
77	15	51.7	6	2	AAW43145 Peptide #
78	15	51.7	6	3	AAV50659 Alphasai-pr
79	15	51.7	6	3	AAV91891 Peptide 6
80	15	51.7	6	5	AAU78502 Gamma sec
81	15	51.7	6	5	ABB08057 Human pce
82	15	51.7	6	5	ABG98337 Secreted
83	15	51.7	6	8	ADN65991 Human 273
84	15	51.7	6	8	ADN05582 Antipsori
85	15	51.7	6	8	ADO04697 Human int
86	15	51.7	7	2	AAR26356 Fungicida
87	15	51.7	7	2	AAR26357 Fungicida
88	15	51.7	7	2	AAR26354 Fungicida
89	15	51.7	7	2	AAR26353 Fungicida
90	15	51.7	7	2	AAR26349 Fungicida
91	15	51.7	7	5	ABB83038 Transferr
92	15	51.7	7	5	ABG77666 Targettin
93	15	51.7	7	7	ADB79562 Parapoxvi
94	15	51.7	7	7	ADB33536 APP gamma
95	15	51.7	7	7	ADG64518 Family A
96	15	51.7	7	7	ADG64331 Thermosta
97	15	51.7	7	8	ADH96974 S. pneumo
98	15	51.7	7	8	ADK72039 Antimicro

99 15 51.7 7 8 ADP74973 Parapoxvi  
100 15 51.7 7 8 ADR72658 Human mon

## ALIGNMENTS

RESULT 1  
AAB30897  
ID AAB30897 standard; peptide; 7 AA.  
XX AC  
XX AAB30897;  
XX DT 02-APR-2001 (first entry)  
XX DE Peptide which selectively binds to normal cardiac endothelium.  
XX KW Cardiac endothelium; angiogenic factor; vascular endothelium;  
XX KW peripheral vascular disease; cardiovascular disease; angiogenesis;  
XX KW cardiac neovascularisation.  
XX OS Unidentified.

XX WO200075329-A1.  
XX PD 14-DEC-2000.  
XX PF 31-MAY-2000; 2000WO-US014988.  
XX PR 07-JUN-1999; 99US-00327045.  
XX PA (EDWA-) EDWARDS LIFESCIENCES CORP.  
XX PA (BAXT ) BAXTER AG.  
XX PI Levine AJ, Mitterer A, Falkner F, Scheiflinger F, Dörner F;  
XX PI WPI; 2001-091212/10.  
XX DR  
XX XX

PT New chimeric molecules having an angiogenic factor linked to a targeting  
PT molecule that binds to a vascular endothelium, useful for increasing  
PT cardiac neovascularization, or treating peripheral vascular and  
PT cardiovascular diseases.

PS Disclosure; Page 27; 67pp; English.

XX AAB30895-99 represent targeting molecules, which are used to produce the  
CC chimeric molecules of the invention. AAB30895-98 selectively bind to  
CC normal cardiac endothelium. The specification describes a chimeric  
CC molecule comprising an angiogenic factor linked to a targeting molecule  
CC that specifically binds to a vascular endothelium. The chimeric molecules  
CC are useful for treatment of peripheral vascular or cardiovascular  
CC diseases. Specifically, they are useful for inducing or inhibiting  
CC angiogenesis, for increasing cardiac neovascularisation in ischemic  
CC tissue in the peripheral vascular system

XX Sequence 7 AA;

Query Match 100.0%; Score 29; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLVTSS 7  
Db 1 VVLVTSS 7

RESULT 2  
AAB50799  
ID AAB50799 standard; peptide; 7 AA.  
XX AC  
XX AAB50799;  
XX DT 21-MAR-2001 (first entry)

XX Heart homing peptide SEQ ID NO: 4.  
DE  
XX  
XX Heart homing peptide; cardiovascular disease; ischaemic disease;  
KW gene therapy.  
XX OS Synthetic.

XX WO200075174-A1.  
XX PD 14-DEC-2000.  
XX PF 31-MAY-2000; 2000WO-US015088.  
XX PR 07-JUN-1999; 99US-00326718.  
XX XX

(BURN-) BURNHAM INST.

XX Ruoslahti E, Mackenna DA;

XX WPI; 2001-071059/08.

XX Novel heart homing peptide that selectively homes to normal ischemic and  
PT cardiac tissue useful for targeting ischemic tissues for treating  
PT ischemic and cardiovascular diseases such as atherosclerosis and  
PT restenosis.

XX Claim 2; Page 55; 70pp; English.

XX The present invention provides a number of heart homing peptides which  
CC selectively home to cardiac tissue. These can be used in the treatment of  
CC cardiovascular and ischaemic diseases, such as atherosclerosis, myocardial  
CC thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial  
CC hypertrophy, congenital heart diseases, ischaemic heart disease and  
CC anginas, acquired valvular/endocardial diseases, primary myocardial  
CC diseases, cardiac tumours and arrhythmias

XX Sequence 7 AA;

Query Match 100.0%; Score 29; DB 4; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VVLVTSS 7  
Db 1 VVLVTSS 7

RESULT 3  
AAW43141  
ID AAW43141 standard; peptide; 6 AA.

XX AAW43141;

XX 31-MAR-1998 (first entry)

XX Anti-melittin peptide #20.

XX Anti-melittin peptide; bee sting; melittin; haemolytic activity;  
KW bee venom; red blood cell; cell lysis; anti-microbial.

XX Synthetic.

XX Key Location/Qualifiers  
XX Modified-site 1  
FT /note= "N-terminally acetylated"  
FT Modified-site 6  
FT /note= "C-terminally amidated"

XX US5698673-A.

XX 16-DEC-1997.

XX

PF 04-MAY-1995; 95US-00434761.  
 PR 18-JUN-1993; 93US-00079445.  
 XX (TORR-) TORREY PINES INST.  
 XX Houghten RA, Pinilla C, Blondelle SE;  
 FI WPI; 1998-051545/05.  
 XX Anti-mellitin peptide(s) - useful for treating bee stings.  
 PT Example 2; Col 32; 26pp; English.  
 PS This sequence represents a specific example of a peptide having anti-mellitin activity with an IC50 value of less than 30 microg/ml. It is useful for treating mellittin poisoning. Mellittin is the active compound in bee venom and causes cell lysis. Peptides having anti-mellittin activity have one of the following formulae; Ac-IVILIZZ-NH2; Ac-IVILTZ-NH2; Ac-IVILIZ-NH2; Ac-IVIPFZ-NH2; Ac-Z1-Z2-I-Z3-Z4-E-NH2; Ac-MILWIE-NH2; Ac-VIOQFV-NH2; Ac-WIQIFI-NH2; where Z= an optionally methylated or chlorinated D-form or natural amino acid; Z1= F or I; Z2= I or Q; Z3= W or Y and Z4= C or F  
 XX Sequence 6 AA;  
 SQ Query Match 65.5%; Score 19; DB 2; Length 6;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 VLVITS 6  
 Db 1 IVILTS 6  
 RESULT 4  
 ADE39237  
 ID ADE39237 standard; peptide; 7 AA.  
 XX ADE39237;  
 AC ADE39237;  
 XX 29-JAN-2004 (first entry)  
 DT Oestrogen receptor-alpha specific monobody peptide seq id 35.  
 DE nuclear receptor antagonist; nuclear receptor agonist;  
 KW fibronectin type III; Fn3; polypeptide monobody;  
 KW nuclear receptor binding activity; drug screening;  
 KW protein activity modulator; lexA; oestrogen receptor alpha; ER-alpha; monobody; motif.  
 XX Synthetic.  
 OS US2003186385-A1.  
 XX 02-OCT-2003.  
 PD 19-NOV-2001; 2001US-00006760.  
 PF 17-NOV-2000; 2000US-0249756P.  
 PR (KOID/) KOIDE S.  
 XX Koide S;  
 FI WPI; 2003-803152/75.  
 DR New fibronectin type III polypeptide monobody useful for screening a candidate drug for nuclear receptor agonist or antagonist activity, and to validate target protein activity.  
 PT Example 2; SEQ ID NO 35; 45pp; English.  
 PS

CC The invention describes a fibronectin type III (Fn3) polypeptide monobody (I) comprising 2 Fn3 beta-strand domain sequences with a loop region sequence linked between adjacent beta-strand domain sequences; and optionally an N-terminal tail of 2 amino acids, a C-terminal tail of 2 amino acids, or both. The loop region sequence, N-terminal tail, or C-terminal tail comprises an amino acid sequence which varies by deletion, insertion, or replacement of 2 amino acids from the corresponding region in a wild-type Fn3 domain of fibronectin, and the monobody exhibits nuclear receptor binding activity. (I) is used to screen a candidate drug for nuclear receptor agonist or antagonist activity, and is used to validate target protein activity. (I) is also used to measure the binding affinity of (I) for a target protein, and can modulate target protein activity. A new method is used to identify (I). (I) can also be used in therapeutics. This is the amino acid sequence of a motif occurring in monobodies selected in the presence of an agonist while using the LexA-oestrogen receptor alpha fusion protein as prey in a two-hybrid assay.  
 XX Sequence 7 AA;  
 SQ Query Match 65.5%; Score 19; DB 7; Length 7;  
 Best Local Similarity 66.7%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 Qy 2 VLVTS 7  
 Db 2 VLITRS 7  
 RESULT 5  
 ADC55448  
 ID ADC55448 standard; peptide; 5 AA.  
 XX ADC55448;  
 AC ADC55448;  
 XX 18-DEC-2003 (first entry)  
 DT Epimorphin activity control oligopeptide #3.  
 DE oligopeptide; epimorphin.  
 KW Unidentified.  
 XX JP2003146998-A.  
 PN 21-MAY-2003.  
 PD 13-NOV-2001; 2001JP-00347339.  
 PF 13-NOV-2001; 2001JP-00347339.  
 PR (SUME) SUMITOMO ELECTRIC IND LTD.  
 XX WPI; 2003-818309/77.  
 DR Novel oligopeptide possessing binding capacity to epimorphin and controlling activity of epimorphin, useful as hair growth retardant and hair growth stimulant.  
 PT Claim 1; SEQ ID NO 3; 11pp; Japanese.  
 XX The present invention relates to an oligopeptide possessing binding capacity to epimorphin, controlling activity of epimorphin. The present sequence is contained in the epimorphin activity control oligopeptide of the invention.  
 CC Sequence 5 AA;  
 SQ Query Match 62.1%; Score 18; DB 7; Length 5;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 Qy 3 LVTS 7  
 Db 3 LVTS 7

```

Db      1 LLTSS 5

RESULT 6
ID      ADC55447
AC      ADC55447 standard; peptide; 6 AA.
XX
XX
AC      ADC55447;
XX
DT      18-DEC-2003 (first entry)
XX
DE      Epimorphin activity control oligopeptide #2.
XX
KW      oligopeptide; epimorphin.
XX
OS      Unidentified.
XX
PN      JP2003146998-A.
XX
PD      21-MAY-2003.
XX
PF      13-NOV-2001; 2001JP-00347339.
XX
PR      13-NOV-2001; 2001JP-00347339.
XX
PA      (SUME ) SUMITOMO ELECTRIC IND LTD.
XX
DR      WPI; 2003-818309/77.
XX
PT      Novel oligopeptide possessing binding capacity to epimorphin and
PT      controlling activity of epimorphin, useful as hair growth retardant and
PT      hair growth stimulant.
XX
PS      Claim 2; SEQ ID NO 2; 11pp; Japanese.
XX
XX
CC      The present invention relates to an oligopeptide possessing binding
CC      capacity to epimorphin, controlling activity of epimorphin. The present
CC      sequence is contained in the epimorphin activity control oligopeptide of
CC      the invention.
XX
SQ      Sequence 6 AA;

Query Match      62.1%; Score 18; DB 7; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.8e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 LVTSS 7
        :|||
Db      1 LLTSS 5

RESULT 7
ID      AAY15720
AC      AAY15720 standard; peptide; 7 AA.
XX
XX
AC      AAY15720;
XX
DT      27-JUL-1999 (first entry)
XX
DE      Peptide used to make fluorescent reporter molecules.
XX
KW      Fluorogenic; fluorescent reporter molecule; enzyme substrate; apoptosis;
KW      protease; peptidase; apoptosis cascade; cancer; chemotherapeutic agent;
KW      cell death; viral protease activity.
XX
XX
OS      Synthetic.
XX
PN      WO9918856-A1.
XX
PD      22-APR-1999.
XX
PF      09-OCT-1998; 98WO-US021231.
XX

PR      10-OCT-1997; 97US-0061582P.
PR      03-MAR-1998; 98US-00033661.
XX
XX      (CYTO-) CYTOVIA INC.
XX
PI      Weber E, Cai SX, Keana JFW, Drewe JA, Zhang H;
XX
XX      WPI; 1999-312448/26.
XX
PT      New fluorogenic or fluorescent reporter molecules.
XX
PS      Disclosure; Page 187; 202pp; English.
XX
XX
CC      AAY15618-Y15759 represent peptides used to make the fluorogenic or
CC      fluorescent reporter molecules of the invention. These molecules contain
CC      a peptide moiety (e.g. present sequence) which acts as a substrate for
CC      enzymes involved in apoptosis or protease or peptidase enzymes. The
CC      compounds can be used as fluorogenic or fluorescent substrates for
CC      enzymes. Depending on the peptide moiety used, the fluorescent molecules
CC      can be used for detecting or measuring the activity of an enzyme involved
CC      in the apoptosis cascade in cells; to determine whether a test compound
CC      has an effect on an enzyme involved in the apoptosis cascade in cells;
CC      for determining the sensitivity of an animal with cancer to treatment
CC      with chemotherapeutic agents or determining whether a test substance
CC      inhibits, prevents, causes or enhances cell death of test cells; for
CC      detecting or measuring the activity of a viral protease in cells; for
CC      determining whether a test compound has an effect on the activity of a
CC      viral protease in cells; and for measuring the activity or determining
CC      whether a test substance has an effect on the activity of a protease or
CC      peptidase in cells
XX
SQ      Sequence 7 AA;

Query Match      62.1%; Score 18; DB 2; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.8e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      1 VVLVTSS 7
        :|||
Db      1 LVLASSS 7

RESULT 8
ID      AAY80874
AC      AAY80874 standard; peptide; 7 AA.
XX
XX
AC      AAY80874;
XX
DT      22-MAY-2000 (first entry)
XX
DE      Fluorophore-labelled protease substrate peptide, SEQ ID NO:103.
XX
KW      Protease substrate; fluorescent label; fluorophore; rhodamine;
KW      blocking group; halobenzoyle group; cleavage; caspase; viral protease;
KW      methionine aminopeptidase type 2; MetAP-2; drug screening.
XX
XX
OS      Synthetic.
XX
PN      WO200004914-A1.
XX
PD      03-FEB-2000.
XX
PF      21-JUL-1999; 99WO-US016423.
XX
PR      21-JUL-1998; 98US-0093642P.
XX
XX      (CYTO-) CYTOVIA INC.
XX      (ZHAN/) ZHANG H.
XX      (CAIS/) CAI S X.
XX      (DREW/) DREWE J A.
XX      (YANG/) YANG W.
XX
PI      Zhang H, Cai SX, Drewe JA, Yang W;

```

XX WPI; 2000-195079/17.  
 XX New fluorescently labeled amino acids or peptides, used as substrates for  
 PT detecting enzymes or their modulators, e.g. anticancer or antiviral  
 PT agents, contains a halobenzoyl N-blocking group.  
 XX Claim 33; Page 111; 174pp; English.  
 XX The invention relates to fluorescently labelled peptides containing a  
 CC halobenzoyl group on the fluorophore. They are of the structure peptide-Y  
 CC -Z, where Z represents a halo-substituted benzoyl blocking group, Y is a  
 CC fluorescent or fluorogenic moiety (preferably a rhodamine), and the  
 CC peptide-Y bond is cleavable by the enzyme being assayed. The labelled  
 CC peptides are reporters for detecting intracellular proteolytic enzymes,  
 CC particularly caspases and other enzymes involved in apoptosis; viral  
 CC proteases (e.g., HIV, herpes simplex virus-1, human cytomegalovirus and  
 CC hepatitis C virus proteases); and methionine aminopeptidase type 2 (MetAP  
 CC -2). The peptides are particularly used to identify modulators of these  
 CC enzymes which may be potentially useful as agents for treating conditions  
 CC such as cancer, neurodegeneration, autoimmune diseases, myocardial  
 CC infarction and viral infection. Modulators identified may also be used to  
 CC prolong the life of cells being cultured for recombinant protein  
 CC production, or to monitor the treatment of cancer with chemotherapeutic  
 CC agents. Inhibitors of MetAP-2 are potential anti- angiogenic or  
 CC anticancer agents. Sequences AAY80782-Y80910 represent peptides, some of  
 CC which are specifically claimed, which may be used in assay methods  
 CC according to the invention  
 XX Sequence 7 AA;  
 SQ

Query Match 62.1%; Score 18; DB 3; Length 7;  
 Best Local Similarity 57.1%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 VLVLTSS 7  
 DB :|| :||  
 1 LVLASS 7

RESULT 9  
 ADC55446  
 ID ADC55446 standard; peptide; 7 AA.  
 XX  
 AC ADC55446;  
 XX  
 DT 18-DEC-2003 (first entry)  
 XX  
 DE Epimorphin activity control oligopeptide #1.  
 XX  
 KW oligopeptide; epimorphin.  
 XX  
 OS Unidentified.  
 XX  
 PN JP2003146998-A.  
 XX  
 XX 21-MAY-2003.  
 XX  
 PF 13-NOV-2001; 2001JP-00347339.  
 XX  
 PR 13-NOV-2001; 2001JP-00347339.  
 XX  
 XX (SUME ) SUMITOMO ELECTRIC IND LTD.  
 PA  
 XX WPI; 2003-818309/77.  
 DR  
 XX Novel oligopeptide possessing binding capacity to epimorphin and  
 PT controlling activity of epimorphin, useful as hair growth retardant and  
 PT hair growth stimulant.  
 PT  
 XX Claim 2; SEQ ID NO 1; 11pp; Japanese.  
 PS  
 XX The present invention relates to an oligopeptide possessing binding  
 CC

CC capacity to epimorphin, controlling activity of epimorphin. The present  
 CC sequence is contained in the epimorphin activity control oligopeptide of  
 CC the invention.  
 XX  
 SQ Sequence 7 AA;  
 Query Match 62.1%; Score 18; DB 7; Length 7;  
 Best Local Similarity 80.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;  
 QY 3 LVTSS 7  
 DB |:|||  
 1 LVTSS 5

RESULT 10  
 AAR34100  
 ID AAR34100 standard; peptide; 4 AA.  
 XX  
 AC AAR34100;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 05-AUG-1993 (first entry)  
 XX  
 DE Peptide which binds the ICAM-1 binding site on IRBC.  
 XX  
 KW Immunoadhesin; Plasmodium falciparum infected erythrocyte; CD36; malaria;  
 KW intercellular adhesion molecule; ICAM-1; CD54; endothelial receptor;  
 KW antibody.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO9306848-A1.  
 XX  
 PD 15-APR-1993.  
 XX  
 PF 05-OCT-1992; 92WO-US008482.  
 XX  
 PR 03-OCT-1991; 91US-00769625.  
 PR 03-APR-1992; 92US-00862708.  
 PR 12-JUN-1992; 92US-00899061.  
 XX  
 PA (BLOO-) CENT BLOOD RES.  
 XX  
 XX Staunton DE, Springer TA;  
 PI  
 XX WPI; 1993-134130/15.  
 DR  
 XX Inhibition of CD36 binding to malaria infected erythrocytes - by  
 PT administering an antibody covalently attached to CD36 or CD36 fragment,  
 PT useful in diagnosis or treatment of PLASMODIUM FALCIPARUM malaria.  
 XX  
 PS Disclosure; Page 49; 66pp; English.  
 XX  
 XX The peptide AAR34099 is capable of binding the ICAM-1 binding site on an  
 CC IRBC. See related patents WO9306849 and WO9306850. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 XX  
 SQ Sequence 4 AA;  
 Query Match 58.6%; Score 17; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VLVLT 5  
 DB |:|||  
 1 VLVLT 4

RESULT 11  
 AAR34038  
 ID AAR34038 standard; peptide; 4 AA.  
 XX

AC AAR34038;  
 XX  
 XX 25-MAR-2003 (revised)  
 DT 09-JAN-2003 (revised)  
 DT 06-AUG-1993 (first entry)  
 XX  
 XX Peptide which binds the ICAM-1 binding site on IRBC.  
 DE  
 XX Immunoadhesin; Plasmodium falciparum infected erythrocyte; IRBC; malaria;  
 KW intercellular adhesion molecule; ICAM-1; CD54; endothelial receptor;  
 KW antibody.  
 XX  
 XX Unidentified.  
 OS  
 XX WO9306849-A1.  
 PN  
 XX 15-APR-1993.  
 PD  
 XX 05-OCT-1992; 92WO-US008483.  
 PF  
 XX 03-OCT-1991; 91US-00769625.  
 PR  
 XX 03-APR-1992; 92US-00862708.  
 PR  
 XX 12-JUN-1992; 92US-00899064.  
 PR  
 XX (BLOO-) CENT BLOOD RES.  
 PA (USSA ) US SEC OF ARMY.  
 PA  
 XX Staunton DE, Springer TA, Ockenhouse CF;  
 PI  
 XX WPI; 1993-134131/16.  
 DR  
 XX Inhibition of CD36 binding to malaria infected erythrocytes - by admin of  
 PT CD36 or suitable fragment antibody etc.; useful in diagnosis and  
 PT treatment of PLASMODIUM FALCIPARUM malaria.  
 XX  
 XX Disclosure; Page 46; 62pp; English.  
 PS  
 XX The peptide AAR34038 is capable of binding the ICAM-1 binding site on an  
 CC IRBC. See related patents WO9306848 and WO9306850. (Updated on 09-JAN-  
 CC 2003 to add missing OS field.) (Updated on 25-MAR-2003 to correct PN  
 CC field.)  
 XX  
 XX Sequence 4 AA;  
 SQ  
 Query Match 58.6%; Score 17; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VLVT 5  
 DB 1 VLVT 4  
 XX  
 XX Peptide which binds the ICAM-1 binding site on IRBC.  
 DE  
 XX Immunoadhesin; Plasmodium falciparum infected erythrocyte; IRBC; malaria;  
 KW intercellular adhesion molecule; ICAM-1; CD54; endothelial receptor;  
 KW antibody.  
 XX  
 XX Homo sapiens.  
 OS  
 XX WO9306850-A1.  
 PN  
 XX 15-APR-1993.  
 PD

XX 05-OCT-1992; 92WO-US008484.  
 PF  
 XX 03-OCT-1991; 91US-00769625.  
 PR  
 XX 03-APR-1992; 92US-00862708.  
 PR  
 XX 12-JUN-1992; 92US-00899063.  
 PR  
 XX (BLOO-) CENT BLOOD RES.  
 PA (USSA ) US SEC OF ARMY.  
 PA  
 XX Staunton DE, Springer TA, Ockenhouse CF;  
 PI  
 XX WPI; 1993-134132/16.  
 DR  
 XX Inhibition of ICAM-1 binding to malaria-infected erythrocytes - by admin.  
 PT of ICAM-1 or fragment, antibody etc.; useful in diagnosis or treatment of  
 PT PLASMODIUM FALCIPARUM malaria.  
 XX  
 XX Claim 9; Page 49; 67pp; English.  
 PS  
 XX The peptide AAR34090 is capable of binding the ICAM-1 binding site on an  
 CC IRBC. See related patents WO9306848 and WO9306849. (Updated on 25-MAR-  
 CC 2003 to correct PN field.)  
 CC  
 XX Sequence 4 AA;  
 SQ  
 Query Match 58.6%; Score 17; DB 2; Length 4;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 2 VLVT 5  
 DB 1 VLVT 4  
 XX  
 XX RESULT 13  
 AAAB16520  
 ID AAB16520 standard; peptide; 5 AA.  
 XX  
 XX AAB16520;  
 AC  
 XX 27-OCT-2000 (first entry)  
 DT  
 XX  
 XX Angiogenesis-inhibiting protein receptor peptide fragment SEQ ID # 111.  
 DE  
 XX Angiogenesis-inhibiting protein receptor; angiogenesis; angiotatin;  
 KW endostatin; plasminogen; laminin; treatment; wound healing; solid tumour;  
 KW psoriasis; scleroderma; myocardial angiogenesis; Crohn's disease;  
 KW cerebral collateral; arteriovenous malformation; rubecosis; cancer;  
 KW diabetic retinopathy; arthritis; wound healing; peptic ulcer;  
 KW Helicobacter related disease; fracture; cat scratch fever.  
 XX  
 XX Synthetic.  
 OS  
 XX WO200032631-A2.  
 PN  
 XX 08-JUN-2000.  
 PD  
 XX 06-DEC-1999; 99WO-US028897.  
 PF  
 XX 04-DEC-1998; 98US-00206059.  
 PR  
 XX (ENTR-) ENTREMED INC.  
 PA  
 XX Macdonald NJ, Sim KL;  
 PI  
 XX WPI; 2000-412290/35.  
 DR  
 XX New angiogenesis-inhibiting protein receptors, useful in methods for  
 PT treating diseases and processes that are mediated by angiogenesis, such  
 PT as solid tumors, psoriasis, scleroderma and myocardial angiogenesis.  
 XX  
 XX Claim 1; Page 52; 100pp; English.  
 PS



XX This invention relates to angiogenesis-inhibiting protein receptors, and  
 CC the DNA sequences encoding them. Angiogenesis is the generation of new  
 CC blood vessels into a tissue, and normally occurs in wound healing, foetal  
 CC and embryonal development and the formation of the corpus luteum,  
 CC endometrium and placenta. Angiostatin is a protein (see AAB16450 and  
 CC AAB68202) involved in angiogenesis, and has an amino acid sequence  
 CC similar to that of a plasminogen fragment (see murine plasminogen  
 CC AAB16490). Angiostatin has the ability to inhibit angiogenesis.  
 CC Endostatin is also an angiogenesis inhibiting protein (see AAB16451 and  
 CC AAB68203). Sequences AAB68242 and AAB16522 represent coding and protein  
 CC sequences of human laminin. Laminin is an angiostatin binding protein,  
 CC and some of the peptides of the invention share homology with regions of  
 CC laminin. Peptides AAB16452-B16521 (excluding AAB16490) are the  
 CC angiogenesis-inhibiting protein receptor fragments of the invention. The  
 CC peptides bind either angiostatin or endostatin and can be used in methods  
 CC for treating diseases and processes that are mediated by angiogenesis,  
 CC such as solid tumours, psoriasis, scleroderma, myocardial angiogenesis,  
 CC Crohn's disease, cerebral collaterals, arteriovenous malformations,  
 CC rubeoosis, diabetic retinopathy, arthritis, wound healing, peptic ulcers,  
 CC Helicobacter related diseases, fractures, placental and cat scratch  
 CC fever. They are useful for the detection and prognosis of cancer. DNA  
 CC sequences A628204-A628241 encode the peptides of the invention

XX SQ Sequence 5 AA;

Query Match 58.6%; Score 17; DB 3; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTS 6  
 ||||  
 Db 1 LVTS 4

RESULT 14  
 AAM48891  
 ID AAM48891 standard; peptide; 5 AA.

XX AC AAM48891;

XX DT 04-APR-2002 (first entry)

XX DE Fibrinogen alpha 443 peptide fragment.

XX Human; angiostatin; endostatin; angiogenesis; cancer; metastasis;  
 KW psoriasis; scleroderma; Crohn's disease; corneal disease; retinopathy;  
 KW arthritis; wound healing; Helicobacter pylori; peptic ulcer;  
 KW gene therapy; angiostatin antagonist; endostatin antagonist;  
 KW antiangiogenic; cytostatic; antiarthritic; antiinflammatory;  
 KW cerebroprotective; antidiabetic; virucide; antipyretic; vulnerary;  
 KW gynaecological; cat scratch fever.

XX OS Unidentified.

XX PN WO200193897-A2.

XX PD 13-DEC-2001.

XX PF 04-JUN-2001; 2001WO-US017947.

XX PR 02-JUN-2000; 2000US-0209065P.

XX PR 08-MAY-2001; 2001US-0289387P.

XX PA (ENTR-) ENTREMED INC.

XX PI Sim KL, Macdonald NJ;

XX DR WPI; 2002-130569/17.

XX Regulating angiogenesis and treatment of angiogenesis-mediated diseases,  
 PT e.g. hemangioma, tumors or cancer, by administering a tropomyosin binding  
 PT compound or actin disrupting compound.

XX Example 11; Page 63; 95pp; English.

XX The present invention relates to methods of regulating angiogenesis in an  
 CC individual by administering an angiogenesis regulating composition  
 CC comprising a tropomyosin binding compound or an actin disrupting  
 CC compound. The compositions are useful for treating diseases and processes  
 CC mediated by angiogenesis including haemangioma, solid tumours, blood  
 CC borne tumours, leukaemia, metastasis, Crohn's disease, coronary or  
 CC cerebral collaterals, arthritis, diabetic neovascularisation, macular  
 CC degeneration, wound healing, Helicobacter related diseases, ovulation,  
 CC menstruation, and cat scratch fever. The present sequence is a peptide  
 CC described in the exemplification of the invention

XX SQ Sequence 5 AA;

Query Match 58.6%; Score 17; DB 5; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06; Indels 0; Gaps 0;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTS 6  
 ||||  
 Db 1 LVTS 4

RESULT 15

ADD12160

ID ADD12160 standard; peptide; 5 AA.

XX AC ADD12160;

XX DT 01-JAN-2004 (first entry)

XX DE Tumour suppressor/cell viability/critical regulator PL peptide #463.

XX modulator; PDZ; post-synaptic density protein 95; PSD95;  
 KW Drosophila large disc protein; Zonula Occludin 1 protein; ZO-1;  
 KW PDZ ligand; PL; antiinflammatory; antiallergic; antiulcer; antipsoriatic;  
 KW antiaethmatic; dermatological; neuroprotective; virucide; antidiabetic;  
 KW osteopathic; antiarthritic; immunosuppressive; antiatherosclerotic;  
 KW cytostatic; anti-HIV; vasotropic; immunomodulator; neurological disease;  
 KW immune response disease; muscular disease; cancer;  
 KW modulating vesicular trafficking; tumour suppression;  
 KW signal transduction; protein sorting; membrane polarity; apoptosis;  
 KW synapse formation; multi-protein complex; leukocyte activation inhibitor;  
 KW tumour suppressor; cell viability; critical regulator.

XX OS Unidentified.

XX PN WO2003014303-A2.

XX PD 20-FEB-2003.

XX PF 02-AUG-2002; 2002WO-US024655.

XX PR 03-AUG-2001; 2001US-0309841P.

XX PR 25-FEB-2002; 2002US-0360061P.

XX PA (ARBO-) ARBOR VITA CORP.

XX PI Lu PS, Rabinowitz JD, Schweizer J, Carrick DM;

XX DR WPI; 2003-268193/26.

XX Modulator of binding between discs-large homology repeat protein, PDZ and  
 PT PDZ ligand protein, is a peptide having few residues of C-terminal  
 PT sequence of PDZ ligand protein.

XX Disclosure; Page 42; 172pp; English.

XX The invention relates to a novel modulator of binding between a PDZ  
 CC protein (post-synaptic density protein 95 (PSD95), Drosophila large disc  
 CC protein and Zonula Occludin 1 protein (ZO-1)) and a PDZ ligand (PL)

CC protein. The modulator is a peptide having 3 residues of a C-terminal  
 CC sequence of a PL protein. PDZ and PL proteins are a binding pair given in  
 CC specification, or a peptide mimetic of the 3 residue PL protein, or a  
 CC small molecule having similar functional activity as the 3 residue PL  
 CC protein. The reagents of the invention have the following activities:  
 CC antiinflammatory, anti-allergic, antiulcer, antipsoriatic, antiasthmatic,  
 CC dermatological, neuroprotective, virucide, antidiabetic, osteopathic,  
 CC antiarthritic, immunosuppressive, antiatherosclerotic, cytostatic, anti-  
 CC HIV, vasotropic, and immunomodulator. The novel modulator is useful for  
 CC treating a disease correlated with binding between a PDZ protein and PL  
 CC protein. The disease can be a neurological disease, immune response  
 CC disease, muscular disease or cancer. The modulator is useful for  
 CC modulating vesicular trafficking, tumour suppression, signal  
 CC transduction, protein sorting, establishment of membrane polarity,  
 CC apoptosis, regulation of immune response and organisation of synapse  
 CC formation. The modulator is useful for facilitating the assembly of multi  
 CC -protein complexes, often serving as a bridge between several proteins,  
 CC or regulating the function of other proteins, and to inhibit leukocyte  
 CC activation. The modulator is useful for treating diseases characterised  
 CC by inflammatory and humoral immune responses e.g., inflammation, allergy,  
 CC inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma,  
 CC allergic rhinitis, atopic dermatitis, arthritis, multiple sclerosis,  
 CC diabetes, osteoarthritis, graft-versus-host diseases, atherosclerosis,  
 CC leukaemia, infectious diseases (viral infection such as human  
 CC immunodeficiency virus (HIV)), and ischaemia. This sequence represents a  
 CC PL protein C-terminal core peptide of a tumour suppressor, cell  
 CC viability, or critical regulator of the invention.

XX  
 SQ Sequence 5 AA;

Query Match 58.6%; Score 17; DB 7; Length 5;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTS 6  
 ||||  
 Db 1 LVTS 4

Search completed: August 3, 2005, 12:03:14  
 Job time : 100.333 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 11:41:26 ; Search time 25 Seconds  
(without alignments)  
20.902 Million cell updates/sec

Title: US-09-910-582B-4  
Perfect score: 29  
Sequence: 1 VLVVTSS 7

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 61165

Minimum DB seq length: 0  
Maximum DB seq length: 7

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

Issued Patents AA:\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	100.0	7	3	US-09-326-718-4
2	18	62.1	7	3	US-09-357-952-103
3	18	62.1	7	3	US-09-521-650-103
4	18	62.1	7	3	US-09-168-888-103
5	18	62.1	7	4	US-09-947-387-103
6	17	58.6	7	2	US-08-554-591-1
7	16	55.2	6	2	US-08-760-075A-33
8	16	55.2	6	3	US-09-338-546-33
9	16	55.2	6	4	US-09-659-084-33
10	16	55.2	7	3	US-08-840-204-4
11	16	55.2	7	3	US-09-258-754-296
12	16	55.2	7	3	US-09-960-780-75
13	16	55.2	7	3	US-09-042-107-296
14	16	55.2	7	3	US-09-073-898-75
15	16	55.2	7	3	US-09-227-357-410
16	16	55.2	7	3	US-09-298-924-14
17	16	55.2	7	4	US-09-324-494A-4
18	16	55.2	7	4	US-09-312-283C-398
19	16	55.2	7	4	US-09-722-250D-296
20	16	55.2	7	4	US-09-850-351A-75
21	16	55.2	7	4	US-09-676-475A-296
22	15	51.7	5	1	US-08-220-401-19
23	15	51.7	5	2	US-08-437-362-19
24	15	51.7	6	1	US-07-752-101A-9
25	15	51.7	6	1	US-08-079-445-9
26	15	51.7	6	1	US-08-434-761-9
27	15	51.7	6	2	US-09-127-574-39
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					Sequence 14, Appli
					Sequence 398, App
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US-08-351-058A-8  
US-08-798-897-45  
US-08-978-523-45

8  
APR

## ALIGNMENTS

## RESULT 1

US-09-326-718-4  
; Sequence 4, Application US/09326718  
; Patent No. 6303573  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: MacKenna, Deirdre A.  
; TITLE OF INVENTION: Heart Homing Peptides and Methods of  
; TITLE OF INVENTION: Using Same  
; FILE REFERENCE: P-LJ 3512  
; CURRENT APPLICATION NUMBER: US/09/326,718  
; CURRENT FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-326-718-4

Query Match 100.0%; Score 29; DB 3; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7  
Db 1 VLVVTSS 7

## RESULT 2

US-09-357-952-103  
; Sequence 103, Application US/09357952  
; Patent No. 6248904  
; GENERAL INFORMATION:  
; APPLICANT: Zhang, Han-Zhong  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Drewe, John A.  
; APPLICANT: Yang, Wu  
; TITLE OF INVENTION: No. 6248904el Fluorescence Dyes and Their Applications for Whole-  
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Proteases  
; TITLE OF INVENTION: Other Enzymes and the Use Thereof  
; FILE REFERENCE: 1735.0030001  
; CURRENT APPLICATION NUMBER: US/09/357,952  
; CURRENT FILING DATE: 1999-07-21  
; EARLIER APPLICATION NUMBER: US 60/093,642  
; EARLIER FILING DATE: 21-JUL-1998  
; NUMBER OF SEQ ID NOS: 139  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 103  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-357-952-103

Query Match 62.1%; Score 18; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7  
Db 1 VLVVTSS 7

## RESULT 3

US-09-521-650-103  
; Sequence 103, Application US/09521650  
; Patent No. 6395429  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. 6335429el Fluorogenic or Fluorescent Reporter Molecules and  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290002  
; CURRENT APPLICATION NUMBER: US/09/521,650  
; CURRENT FILING DATE: 2000-03-08  
; EARLIER APPLICATION NUMBER: 09/168,888  
; EARLIER FILING DATE: 1998-10-09  
; EARLIER APPLICATION NUMBER: US 60/061,582  
; EARLIER FILING DATE: 1997-10-10  
; EARLIER APPLICATION NUMBER: US 09/033,661  
; EARLIER FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 103  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-521-650-103

Query Match 62.1%; Score 18; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7  
Db 1 VLVVTSS 7

## RESULT 4

US-09-168-888-103  
; Sequence 103, Application US/09168888  
; Patent No. 6342611  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. 6342611el Fluorogenic or Fluorescent Reporter Molecules and  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290002  
; CURRENT APPLICATION NUMBER: US/09/168,888  
; CURRENT FILING DATE: 1998-10-09  
; EARLIER APPLICATION NUMBER: US 60/061,582  
; EARLIER FILING DATE: 1997-10-10  
; EARLIER APPLICATION NUMBER: US 09/033,661  
; EARLIER FILING DATE: 1998-03-03  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 103  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-168-888-103

Query Match 62.1%; Score 18; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

US-09-168-888-103

Query Match 62.1%; Score 18; DB 3; Length 7;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7  
:||:|  
Db 1 LVLASSS 7

RESULT 5

US-09-947-387-103  
; Sequence 103, Application US/09947387  
; Patent No. 6759207  
; GENERAL INFORMATION:  
; APPLICANT: Weber, Eckard  
; APPLICANT: Cai, Sui Xiong  
; APPLICANT: Keana, John F.W.  
; APPLICANT: Drewe, John A.  
; APPLICANT: Zhang, Han-Zhong  
; TITLE OF INVENTION: No. 6759207el Fluorogenic or Fluorescent Reporter Molecules and  
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence  
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the  
; TITLE OF INVENTION: Use Thereof  
; FILE REFERENCE: 1735.0290005  
; CURRENT APPLICATION NUMBER: US/09/947,387  
; PRIOR FILING DATE: 2001-09-07  
; PRIOR APPLICATION NUMBER: US 60/061,582  
; PRIOR FILING DATE: 1997-10-10  
; PRIOR APPLICATION NUMBER: US 60/145,746  
; PRIOR FILING DATE: 1998-03-03  
; PRIOR APPLICATION NUMBER: US 09/168,888  
; PRIOR FILING DATE: 1998-10-09  
; NUMBER OF SEQ ID NOS: 142  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 103  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: Peptide  
US-09-947-387-103

Query Match 62.1%; Score 18; DB 4; Length 7;  
Best Local Similarity 57.1%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVVTSS 7  
:||:|  
Db 1 LVLASSS 7

RESULT 6

US-08-554-591-1  
; Sequence 1, Application US/08554591  
; Patent No. 5834257  
; GENERAL INFORMATION:  
; APPLICANT: Sugano, Yasushi  
; APPLICANT: Terada, Ichiro  
; APPLICANT: Kodama, Hisashi  
; TITLE OF INVENTION: No. 5834257el Alpha-Agarase and Production  
; TITLE OF INVENTION: Process of Oligosaccharides and Monosaccharides  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Birch, Stewart, Kolasch and Birch  
; STREET: P.O. Box 747  
; CITY: Falls Church  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 22040-0747  
; COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: /US/08/554,591  
APPLICATION NUMBER: US/08/554,591  
FILING DATE: 06-NOV-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Murphy Jr., Gerald M  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 1254-124  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 205-8000  
TELEFAX: (703) 205-8050  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-554-591-1

Query Match 58.6%; Score 17; DB 2; Length 7;  
Best Local Similarity 100.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTS 6  
:|:|:  
Db 3 LVTS 6

RESULT 7

US-08-760-075A-33  
; Sequence 33, Application US/08760075A  
; Patent No. 5942429  
; GENERAL INFORMATION:  
; APPLICANT: KIRSCHBAUM, Bernd  
; APPLICANT: MUELINER, Stefan  
; APPLICANT: BARTLETT, Robert  
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: /US/08/760,075A  
APPLICATION NUMBER: US/08/760,075A  
FILING DATE: 04-DEC-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: DE 19545126.0  
FILING DATE: 04-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: GRANADOS, Patricia D.  
REGISTRATION NUMBER: 33,683  
REFERENCE/DOCKET NUMBER: 18748/309  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 33:

; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-760-075A-33

Query Match 55.2%; Score 16; DB 2; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTSS 7  
Db 1 IVTSA 5

RESULT 8  
US-09-338-546-33  
; Sequence 33, Application US/09338546  
; Patent No. 6251645  
; GENERAL INFORMATION:  
; APPLICANT: KIRSCHBAUM, Bernd  
; APPLICANT: MUELLNER, Stefan  
; APPLICANT: BARTLETT, Robert  
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
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; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 04-DEC-1995  
; CLASSIFICATION: US/09/338,546

; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US/08/760,075  
; FILING DATE: 04-DEC-1996  
; APPLICATION NUMBER: DE 19545126.0  
; FILING DATE: 04-DEC-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/309  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-09-338-546-33

Query Match 55.2%; Score 16; DB 3; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTSS 7  
Db 1 IVTSA 5

RESULT 9

US-09-659-084-33  
; Sequence 33, Application US/09659084  
; Patent No. 6403299  
; GENERAL INFORMATION:  
; APPLICANT: KIRSCHBAUM, Bernd  
; APPLICANT: MUELLNER, Stefan  
; APPLICANT: BARTLETT, Robert  
; TITLE OF INVENTION: NOVEL DEAH-BOX PROTEINS  
; NUMBER OF SEQUENCES: 38  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; FILING DATE: 11-Sep-2000  
; CLASSIFICATION: <Unknown>  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 09/338,546  
; FILING DATE: <Unknown>

; ATTORNEY/AGENT INFORMATION:  
; NAME: GRANADOS, Patricia D.  
; REGISTRATION NUMBER: 33,683  
; REFERENCE/DOCKET NUMBER: 18748/309  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 33:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 6 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; SEQUENCE DESCRIPTION: SEQ ID NO: 33:  
US-09-659-084-33

Query Match 55.2%; Score 16; DB 4; Length 6;  
Best Local Similarity 60.0%; Pred. No. 4.1e+05;  
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTSS 7  
Db 1 IVTSA 5

RESULT 10

US-08-840-204-4  
; Sequence 4, Application US/08840204  
; Patent No. 6103498  
; GENERAL INFORMATION:

; APPLICANT: LAWRENCE, DANIEL A.  
; APPLICANT: STEFANSSON, STEINGRIMUR P.  
; TITLE OF INVENTION: MUTANT PLASMINOGEN ACTIVATOR-INHIBITOR  
; TYPE 1 (PAI-1) AND USES THEREOF  
; NUMBER OF SEQUENCES: 10  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORRISON & FOERSTER  
; STREET: 2000 PENNSYLVANIA AVENUE, NW  
; CITY: WASHINGTON  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20006-1812

; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk

;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/840,204  
;; FILING DATE:  
;; CLASSIFICATION: 435  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: LIVNAT, SHMUEL  
;; REGISTRATION NUMBER: 33,949  
;; REFERENCE/DOCKET NUMBER: 30807-20004.00  
;; TELEPHONE: (202) 887-1500  
;; TELEFAX: (202) 822-0168  
;; TELEX: 90-4030 MRSNFOERSWSH  
;; INFORMATION FOR SEQ ID NO: 4:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; US-08-840-204-4

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Best Local Similarity 28.6%; Pred. No. 4.1e+05;  
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVTS 7  
Db 1 MTMTNS 7

RESULT 11  
US-09-258-754-296  
; Sequence 296, Application US/09258754  
; Patent No. 6174687  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Dipeptidase  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 296  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-296

Query Match 55.2%; Score 16; DB 3; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVTSS 7  
Db 2 LVNSS 6

RESULT 12  
US-08-960-780-75  
; Sequence 75, Application US/08960780  
; Patent No. 6204435  
; GENERAL INFORMATION:  
; APPLICANT: Feitelson, Jerald S.  
; APPLICANT: Schnepf, H. Ernest

;; APPLICANT: Narva, Kenneth E.  
;; APPLICANT: Stockhoff, Brian A.  
;; APPLICANT: Schmeits, James  
;; APPLICANT: Loewer, David  
;; APPLICANT: Dullum, Charles Joseph  
;; APPLICANT: Muller-Cohn, Judy  
;; APPLICANT: Stamp, Lisa  
;; TITLE OF INVENTION: No. 6204435el Pesticidal Toxins and Nucleotide  
;; NUMBER OF SEQUENCES: 134  
;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
;; STREET: 2421 N.W. 41st Street, Suite A-1  
;; CITY: Gainesville  
;; STATE: FL  
;; COUNTRY: US  
;; ZIP: 32606-6669  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: Floppy disk  
;; COMPUTER: IBM PC compatible  
;; OPERATING SYSTEM: PC-DOS/MS-DOS  
;; SOFTWARE: PatentIn Release #1.0, Version #1.30  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/960,780  
;; FILING DATE: 30-OCT-1997  
;; CLASSIFICATION: 435  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: US 60/029,848  
;; FILING DATE: 30-OCT-1996  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Saliwanchik, David R.  
;; REGISTRATION NUMBER: 31,794  
;; REFERENCE/DOCKET NUMBER: MA-708  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: 352-375-8100  
;; TELEFAX: 352-372-5800  
;; INFORMATION FOR SEQ ID NO: 75:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 7 amino acids  
;; TYPE: amino acid  
;; STRANDEDNESS: single  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: peptide  
;; US-08-960-780-75

Query Match 55.2%; Score 16; DB 3; Length 7;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLVTS 7  
Db 2 LLSTSS 7

RESULT 13  
US-09-042-107-296  
; Sequence 296, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 296  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-296

Query Match 55.2%; Score 16; DB 3; Length 7;  
Best Local Similarity 80.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 3 LVTSS 7  
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Db 2 LVNSS 6

## RESULT 14

US-09-073-898-75  
; Sequence 75, Application US/09073898  
; Patent No. 6242669

## ; GENERAL INFORMATION:

; APPLICANT: Fietelson, Jerald S.  
; APPLICANT: Schnepf, H. Ernest  
; APPLICANT: Narva, Kenneth E.  
; APPLICANT: Stockhoff, Brian A.  
; APPLICANT: Schmeits, James  
; APPLICANT: Loewer, David  
; APPLICANT: Dullum, Charles Joseph  
; APPLICANT: Muller-Cohn, Judy  
; APPLICANT: Stamp, Lisa  
; APPLICANT: Morrill, George  
; APPLICANT: Finstad-Lee, Stacey  
; TITLE OF INVENTION: No. 6242669el Pesticidal Toxins and Nucleotide  
; TITLE OF INVENTION: Sequences Which Encode These Toxins  
; NUMBER OF SEQUENCES: 144  
; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Saliwanchik, Lloyd & Saliwanchik  
; STREET: 2421 N.W. 41st Street, Suite A-1  
; CITY: Gainesville  
; STATE: FL  
; COUNTRY: US

; ZIP: 32606-6669

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/073,898

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/029,848

; FILING DATE: 30-OCT-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/960,780

; FILING DATE: 30-OCT-1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Sanders, Jay M.

; REGISTRATION NUMBER: 39,355

; REFERENCE/DOCKET NUMBER: MA-708C1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 352-375-8100

; TELEFAX: 352-372-5800

; INFORMATION FOR SEQ ID NO: 75:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 7 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: peptide

US-09-073-898-75

Query Match 55.2%; Score 16; DB 3; Length 7;  
Best Local Similarity 66.7%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLVTS 7  
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Db 2 LLSTSS 7

## RESULT 15

US-09-227-357-410  
; Sequence 410, Application US/09227357  
; Patent No. 6342581  
; GENERAL INFORMATION:  
; APPLICANT: Fischer et al.  
; TITLE OF INVENTION: 123 Human Secreted Proteins  
; FILE REFERENCE: PZ010P1

; CURRENT APPLICATION NUMBER: US/09/227,357

; CURRENT FILING DATE: 1999-01-08

; EARLIER APPLICATION NUMBER: PCT/US98/13684

; EARLIER FILING DATE: 1998-07-07

; EARLIER APPLICATION NUMBER: 60/051,926

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,793

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,925

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,929

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,803

; EARLIER FILING DATE: 1997-07-08

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; EARLIER FILING DATE: 1997-07-08

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; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,916

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,930

; EARLIER FILING DATE: 1997-07-08

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; EARLIER APPLICATION NUMBER: 60/051,920

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; EARLIER APPLICATION NUMBER: 60/052,733

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/052,795

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,919

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/051,928

; EARLIER FILING DATE: 1997-07-08

; EARLIER APPLICATION NUMBER: 60/055,722

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,723

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,948

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,949

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,953

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,950

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,947

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,964

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/056,360

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,684

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,984

; EARLIER FILING DATE: 1997-08-18

; EARLIER APPLICATION NUMBER: 60/055,954

; EARLIER FILING DATE: 1997-08-18



; EARLIER APPLICATION NUMBER: 60/058,785  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,664  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,660  
; EARLIER FILING DATE: 1997-09-12  
; EARLIER APPLICATION NUMBER: 60/058,661  
; EARLIER FILING DATE: 1997-09-12  
; NUMBER OF SEQ ID NOS: 672  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 410  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-227-357-410

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Best Local Similarity 100.0%; Pred.No. 4.1e+05;  
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 4 VLV 7

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Copyright (c) 1993 - 2005 Compugen Ltd.

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(without alignments)  
30.529 Million cell updates/sec

Title: US-09-910-582B-4

Perfect score: 29

Sequence: 1 VLVITSS 7

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Maximum DB seq length: 7

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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2	29	100.0	7	10	US-09-910-582B-4
3	29	100.0	7	17	US-10-838-289-36
4	19	65.5	7	14	US-10-006-760-35
5	18	62.1	7	9	US-09-947-387-103
6	18	62.1	7	15	US-10-138-375-103
7	18	62.1	7	16	US-10-829-381-103
8	17	58.6	5	9	US-09-873-676-111
9	17	58.6	6	15	US-10-363-208-259
10	17	58.6	6	16	US-10-363-204-74
11	17	58.6	7	14	US-10-022-066-209
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					Sequence 4, Appli
					Sequence 35, Appl
					Sequence 36, Appl
					Sequence 103, App
					Sequence 103, App
					Sequence 103, App
					Sequence 111, App
					Sequence 259, App
					Sequence 74, Appl
					Sequence 209, App

12	55.2	7	9	US-09-850-351A-75	Sequence 75, Appl
13	55.2	7	10	US-09-983-802-410	Sequence 410, App
14	55.2	7	10	US-09-866-050A-398	Sequence 398, App
15	55.2	7	10	US-09-984-490-410	Sequence 410, App
16	55.2	7	11	US-09-973-278-637	Sequence 637, App
17	55.2	7	14	US-10-091-724-19	Sequence 19, Appl
18	55.2	7	15	US-10-259-609-4	Sequence 4, Appli
19	55.2	7	15	US-10-431-048-19	Sequence 19, Appl
20	55.2	7	16	US-10-688-276-14	Sequence 14, Appl
21	55.2	7	17	US-10-808-187-2335	Sequence 2335, Ap
22	55.2	7	17	US-10-838-289-96	Sequence 96, Appl
23	55.2	7	17	US-10-607-595-296	Sequence 296, App
24	51.7	5	16	US-10-478-981-72	Sequence 72, Appl
25	51.7	5	17	US-10-808-187-718	Sequence 718, App
26	51.7	6	14	US-10-353-174-25	Sequence 25, Appl
27	51.7	6	16	US-10-399-162-15	Sequence 15, Appl
28	51.7	6	16	US-10-343-389A-4	Sequence 4, Appli
29	51.7	6	16	US-10-641-633-87	Sequence 87, Appl
30	51.7	6	18	US-10-810-881A-131	Sequence 131, App
31	51.7	6	20	US-11-006-372-25	Sequence 25, Appl
32	51.7	7	9	US-09-950-313-46	Sequence 46, Appl
33	51.7	7	15	US-10-401-403-9	Sequence 9, Appli
34	51.7	7	15	US-10-401-403-203	Sequence 203, App
35	51.7	7	17	US-10-808-187-83	Sequence 83, Appl
36	51.7	7	18	US-10-990-767-11	Sequence 11, Appl
37	48.3	4	14	US-10-292-896-7	Sequence 7, Appli
38	48.3	5	8	US-08-859-699-18	Sequence 18, Appl
39	48.3	5	9	US-09-984-183-14	Sequence 14, Appl
40	48.3	5	9	US-09-984-333-4	Sequence 4, Appli
41	48.3	5	14	US-10-292-896-5	Sequence 5, Appli
42	48.3	5	15	US-10-394-980-322	Sequence 322, App
43	48.3	6	9	US-09-782-980-98	Sequence 98, Appl
44	48.3	6	9	US-09-782-980-120	Sequence 120, App
45	48.3	6	9	US-09-956-625-9	Sequence 9, Appli
46	48.3	6	9	US-09-947-387-104	Sequence 104, App
47	48.3	6	9	US-09-071-838-14	Sequence 14, Appl
48	48.3	6	9	US-09-727-963A-56	Sequence 56, Appl
49	48.3	6	9	US-09-727-963A-82	Sequence 82, Appl
50	48.3	6	13	US-10-156-820-52	Sequence 52, Appl
51	48.3	6	14	US-10-165-844-26	Sequence 26, Appl
52	48.3	6	14	US-10-213-512-14	Sequence 14, Appl
53	48.3	6	14	US-10-319-402-28	Sequence 28, Appl
54	48.3	6	15	US-10-138-375-104	Sequence 104, App
55	48.3	6	15	US-10-414-524-112	Sequence 112, App
56	48.3	6	16	US-10-806-018-98	Sequence 98, Appl
57	48.3	6	16	US-10-806-018-120	Sequence 120, App
58	48.3	6	16	US-10-829-381-104	Sequence 104, App
59	48.3	6	17	US-10-808-187-1360	Sequence 1360, Ap
60	48.3	6	17	US-10-808-187-1621	Sequence 1621, Ap
61	48.3	6	17	US-10-901-243-16	Sequence 16, Appl
62	48.3	6	17	US-10-728-246-24	Sequence 24, Appl
63	48.3	6	17	US-10-715-810-64	Sequence 64, Appl
64	48.3	6	17	US-10-684-346-19	Sequence 19, Appl
65	48.3	6	17	US-10-666-095-15	Sequence 15, Appl
66	48.3	7	10	US-09-954-385-243	Sequence 243, App
67	48.3	7	10	US-09-954-385-429	Sequence 429, App
68	48.3	7	11	US-09-833-245-725	Sequence 725, App
69	48.3	7	14	US-10-267-849-40	Sequence 40, Appl
70	48.3	7	14	US-10-044-692-142	Sequence 142, App
71	48.3	7	14	US-10-044-539-142	Sequence 142, App
72	48.3	7	14	US-10-133-210-247	Sequence 247, App
73	48.3	7	14	US-10-319-402-8	Sequence 8, Appli
74	48.3	7	14	US-10-319-402-30	Sequence 30, Appl
75	48.3	7	14	US-10-006-760-39	Sequence 39, Appl
76	48.3	7	14	US-10-367-599-7	Sequence 7, Appli
77	48.3	7	15	US-10-325-810-375	Sequence 375, App
78	48.3	7	15	US-10-243-613-7	Sequence 7, Appli
79	48.3	7	16	US-10-727-335-36	Sequence 36, Appl
80	48.3	7	16	US-10-877-124-375	Sequence 375, App
81	48.3	7	16	US-10-877-022-375	Sequence 375, App
82	48.3	7	17	US-10-877-146-375	Sequence 375, App
83	48.3	7	17	US-10-901-243-15	Sequence 15, Appl
84	48.3	7	17	US-10-912-512-243	Sequence 243, App

85 14 48.3 7 17 US-10-912-512-429 Sequence 429, App  
86 14 48.3 7 17 US-10-235-043-243 Sequence 243, App  
87 14 48.3 7 17 US-10-235-043-429 Sequence 429, App  
88 14 48.3 7 17 US-10-496-507-3 Sequence 3, Appl  
89 13 44.8 4 9 US-09-769-145-59 Sequence 59, Appl  
90 13 44.8 4 9 US-09-264-516A-20 Sequence 20, Appl  
91 13 44.8 4 9 US-09-185-908-3 Sequence 3, Appl  
92 13 44.8 4 10 US-09-910-706A-15 Sequence 15, Appl  
93 13 44.8 4 14 US-10-105-008-59 Sequence 59, Appl  
94 13 44.8 4 14 US-10-006-869-432 Sequence 432, App  
95 13 44.8 4 14 US-10-058-821-39 Sequence 39, Appl  
96 13 44.8 4 14 US-10-141-357-20 Sequence 20, Appl  
97 13 44.8 4 14 US-10-222-455-36 Sequence 36, Appl  
98 13 44.8 4 15 US-10-359-546-67 Sequence 67, Appl  
99 13 44.8 4 15 US-10-395-032-432 Sequence 432, App  
100 13 44.8 4 15 US-10-425-557-59 Sequence 59, Appl

## ALIGNMENTS

RESULT 1  
US-09-782-650-3  
; Sequence 3, Application US/09782650  
; Patent No. US20020019350A1  
; GENERAL INFORMATION:  
; APPLICANT: Levine, Arnold J.  
; APPLICANT: Mitterer, Artur  
; APPLICANT: Falkner, Falko-Gunter  
; APPLICANT: Scheiflinger, Friedrich  
; APPLICANT: Dörner, Friedrich  
; APPLICANT: Edwards Lifesciences Corporation  
; TITLE OF INVENTION: Targeted Angiogenesis  
; FILE REFERENCE: 20553D-000611US  
; CURRENT APPLICATION NUMBER: US/09/782.650  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR FILING DATE: 2001-02-12  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: US 09/324,079  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: US 09/327,045  
; PRIOR FILING DATE: 1999-06-07  
; PRIOR APPLICATION NUMBER: PCT/US00/14988  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 3  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:targeting  
; OTHER INFORMATION: molecule  
US-09-782-650-3

Query Match 100.0%; Score 29; DB 9; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVLTSS 7  
| | | | |  
DB 1 VLVLTSS 7

RESULT 2  
US-09-910-582B-4  
; Sequence 4, Application US/09910582B  
; Publication No. US20030045476A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Mackenna, Deirdre A.  
; TITLE OF INVENTION: Heart Homing Conjugates  
; FILE REFERENCE: P-LJ 4857  
; CURRENT APPLICATION NUMBER: US/09/910,582B  
; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/326,718  
; PRIOR FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 4  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-910-582B-4

Query Match 100.0%; Score 29; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVLTSS 7  
| | | | |  
DB 1 VLVLTSS 7

RESULT 3  
US-10-838-289-36  
; Sequence 36, Application US/10838289  
; Publication No. US20050058603A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Jimming  
; APPLICANT: Ai, Hua  
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
; TITLE OF INVENTION: NANOSHELLS  
; FILE REFERENCE: CMRU-P01-040  
; CURRENT APPLICATION NUMBER: US/10/838,289  
; CURRENT FILING DATE: 2004-05-03  
; PRIOR APPLICATION NUMBER: US 60/502,429  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: US 60/467,389  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 756  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 36  
; LENGTH: 7  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Heart homing peptide  
US-10-838-289-36

Query Match 100.0%; Score 29; DB 17; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VLVLTSS 7  
| | | | |  
DB 1 VLVLTSS 7

RESULT 4  
US-10-006-760-35  
; Sequence 35, Application US/10006760  
; Publication No. US20030186385A1  
; GENERAL INFORMATION:  
; APPLICANT: Koide, Shohel  
; TITLE OF INVENTION: METHOD OF IDENTIFYING POLYPEPTIDE MONOBODIES WHICH BIND  
; TITLE OF INVENTION: TO TARGET PROTEINS AND USE THEREOF  
; FILE REFERENCE: 176/60901  
; CURRENT APPLICATION NUMBER: US/10/006,760  
; CURRENT FILING DATE: 2001-11-19  
; PRIOR APPLICATION NUMBER: 60/249,756  
; PRIOR FILING DATE: 2000-11-17  
; NUMBER OF SEQ ID NOS: 73  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 35  
; LENGTH: 7

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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: AB loop
; OTHER INFORMATION: sequence for polypeptide monobody in pYT45AB7N
; OTHER INFORMATION: library
US-10-006-760-35

Query Match      65.5%; Score 19; DB 14; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 2 VLVTSS 7
Db 2 VLITRS 7

RESULT 5
US-09-947-387-103
; Sequence 103, Application US/09947387
; Patent No. US20020150885A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: No. US20020150885A1el Fluorogenic or Fluorescent Reporter Molecule
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290005
; CURRENT APPLICATION NUMBER: US/09/947,387
; CURRENT FILING DATE: 2001-09-07
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-947-387-103

Query Match      62.1%; Score 18; DB 9; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVTSS 7
Db 1 LVLASS 7

RESULT 6
US-10-138-375-103
; Sequence 103, Application US/10138375
; Publication No. US20030208037A1
; GENERAL INFORMATION:
; APPLICANT: Zhang, Han-Zhong
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Drewe, John A.
; APPLICANT: Yang, Wu
; TITLE OF INVENTION: No. US20030208037A1el Fluorescence Dyes and Their Applications for
; TITLE OF INVENTION: Fluorescence Screening Assays for Caspases, Peptidases, Protease
; TITLE OF INVENTION: Other Enzymes and the Use Thereof
; FILE REFERENCE: 1735.0030001
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; CURRENT APPLICATION NUMBER: US/10/138,375
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/357,952
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-21
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/093,642
; PRIOR FILING DATE: EARLIER FILING DATE: 21-JUL-1998
; NUMBER OF SEQ ID NOS: 139
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-138-375-103

Query Match      62.1%; Score 18; DB 15; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVTSS 7
Db 1 LVLASS 7

RESULT 7
US-10-829-381-103
; Sequence 103, Application US/10829381
; Publication No. US20040191844A1
; GENERAL INFORMATION:
; APPLICANT: Weber, Eckard
; APPLICANT: Cai, Sui Xiong
; APPLICANT: Keana, John F.W.
; APPLICANT: Drewe, John A.
; APPLICANT: Zhang, Han-Zhong
; TITLE OF INVENTION: Novel Fluorogenic or Fluorescent Reporter Molecules and
; TITLE OF INVENTION: Their Applications for Whole-Cell Fluorescence
; TITLE OF INVENTION: Screening Assays for Caspases and Other Enzymes and the
; TITLE OF INVENTION: Use Thereof
; FILE REFERENCE: 1735.0290006
; CURRENT APPLICATION NUMBER: US/10/829,381
; CURRENT FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/061,582
; PRIOR FILING DATE: 1997-10-10
; PRIOR APPLICATION NUMBER: US 60/145,746
; PRIOR FILING DATE: 1998-03-03
; PRIOR APPLICATION NUMBER: US 09/168,888
; PRIOR FILING DATE: 1998-10-09
; PRIOR APPLICATION NUMBER: US 09/947,387
; PRIOR FILING DATE: 2001-09-07
; NUMBER OF SEQ ID NOS: 142
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 103
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-10-829-381-103

Query Match      62.1%; Score 18; DB 16; Length 7;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 VLVTSS 7
Db 1 LVLASS 7

RESULT 8
US-09-873-676-111
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; Sequence 111, Application US/09873676
; Patent No. US20020077289A1
; GENERAL INFORMATION:
; APPLICANT: MacDonald, Nicholas J.
; TITLE OF INVENTION: Angiostatin and Endostatin Binding Proteins and Methods of Use
; FILE REFERENCE: 05213-0378 (43170-259333)
; CURRENT APPLICATION NUMBER: US/09/873,676
; CURRENT FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: US 60/209,065
; PRIOR FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 60/289,387
; PRIOR FILING DATE: 2001-05-08
; NUMBER OF SEQ ID NOS: 123
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 111
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic Peptide
; US-09-873-676-111

Query Match      58.6%; Score 17; DB 9; Length 5;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 LVTS 6
Db 1 LVTS 4

RESULT 9
US-10-363-208-259
; Sequence 259, Application US/10363208
; Publication No. US20040048243A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting
; FILE REFERENCE: 005774.P005PCT
; CURRENT APPLICATION NUMBER: US/10/363,208
; CURRENT FILING DATE: 2003-03-07
; NUMBER OF SEQ ID NOS: 273
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 259
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(6)
; OTHER INFORMATION: synthetic construct
; US-10-363-208-259

Query Match      58.6%; Score 17; DB 15; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLVT 5
Db 2 VLVT 5

RESULT 10
US-10-363-204-74
; Sequence 74, Application US/10363204
; Publication No. US20040170955A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents, The University of Texas System
; TITLE OF INVENTION: Human and Mouse Targeting Peptides Identified by Phage Display
; FILE REFERENCE: 005774.P003PCT
; CURRENT APPLICATION NUMBER: US/10/363,204
; CURRENT FILING DATE: 2003-03-07

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; NUMBER OF SEQ ID NOS: 251
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 74
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(6)
; OTHER INFORMATION: synthetic construct
; US-10-363-204-74

Query Match      58.6%; Score 17; DB 16; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 VLVT 5
Db 2 VLVT 5

RESULT 11
US-10-022-066-209
; Sequence 209, Application US/10022066
; Publication No. US20030166057A1
; GENERAL INFORMATION:
; APPLICANT: HILDEBRAND, WILLIAM H.
; APPLICANT: PRILLMAN, KILEY RAE
; TITLE OF INVENTION: METHOD AND APPARATUS FOR THE PRODUCTION OF ANTIGENS AND
; TITLE OF INVENTION: USES THEREOF
; FILE REFERENCE: 6680.034
; CURRENT APPLICATION NUMBER: US/10/022,066
; CURRENT FILING DATE: 2002-09-09
; PRIOR APPLICATION NUMBER: 60/256,410
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 60/256,409
; PRIOR FILING DATE: 2000-12-18
; PRIOR APPLICATION NUMBER: 09/465,321
; PRIOR FILING DATE: 1999-12-17
; PRIOR APPLICATION NUMBER: 09/974,366
; PRIOR FILING DATE: 2001-10-10
; NUMBER OF SEQ ID NOS: 638
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 209
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
; US-10-022-066-209

Query Match      58.6%; Score 17; DB 14; Length 7;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VVLVTS 6
Db 1 LVIVTT 6

RESULT 12
US-09-850-351A-75
; Sequence 75, Application US/09850351A
; Patent No. US2002010080A1
; GENERAL INFORMATION:
; APPLICANT: Feitelson, Jerald S.
; APPLICANT: Schnepf, H. Ernest
; APPLICANT: Narva, Kenneth E.
; APPLICANT: Stockhoff, Brian A.
; APPLICANT: Schmeits, James
; APPLICANT: Loewer, David
; APPLICANT: Dullum, Charles Joseph

```

Query Match 55.2%; Score 16; DB 10; Length 7;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 0; Mismatches 0; Indels  
QY 1 VVLV 4

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Db      |||||
        4 VLVV 7

RESULT 14
US-09-866-050A-398
; Sequence 398, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Onrust, Rene
; APPLICANT: Murison, James G.
; APPLICANT: Kumble, Krishanand D.
; TITLE OF INVENTION: Compositions Isolated From Skin Cells
; FILE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c4U
; CURRENT APPLICATION NUMBER: US/09/866,050A
; CURRENT FILING DATE: 2001-05-24
; NUMBER OF SEQ ID NOS: 725
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 398
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Mouse
US-09-866-050A-398

Query Match      55.2%; Score 16; DB 10; Length 7;
Best Local Similarity 33.3%; Pred. No. 1.6e+06;
Matches 2; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLVVTS 6
        :|::|||
Db      1 MVIIT 6

RESULT 15
US-09-984-490-410
; Sequence 410, Application US/09984490
; Publication No. US20030064412A1
; GENERAL INFORMATION:
; APPLICANT: Fischer et al.
; TITLE OF INVENTION: 123 Human Secreted Proteins
; FILE REFERENCE: P2010P1
; CURRENT APPLICATION NUMBER: US/09/984,490
; CURRENT FILING DATE: 2001-10-30
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/227,357
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
; PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08

Query Match      55.2%; Score 16; DB 10; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 VLVV 4
        |||||
Db      4 VLVV 7

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Job time : 91.3333 secs
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:07:52 ; Search time 38 Seconds  
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Title: US-09-910-582B-9  
Perfect score: 51  
Sequence: 1 CLHRGNSC 8

Scoring table: BLOSUM62  
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Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 606

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : PIR 79:\*

1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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5	16	31.4	8	2	C61512
6	16	31.4	8	2	D61512
7	15	29.4	7	4	I55382
8	14	27.5	6	2	A41946
9	14	27.5	7	2	S45311
10	14	27.5	8	2	S59622
11	14	27.5	8	2	PH1618
12	14	27.5	8	2	A25836
13	14	27.5	8	2	XGHU9U
14	13	25.5	5	2	B22565
15	13	25.5	6	2	C22565
16	13	25.5	6	2	I37263
17	13	25.5	6	2	B56979
18	13	25.5	6	2	I49421
19	13	25.5	7	2	PH1408
20	13	25.5	8	2	B54823
21	13	25.5	8	2	A54823
22	13	25.5	8	2	I57018
23	13	25.5	8	2	S65381
24	13	25.5	8	2	S89195
25	12	23.5	5	2	PT0695
26	12	23.5	6	2	S78764
27	12	23.5	6	2	PT0532
28	12	23.5	6	2	A43129
29	12	23.5	7	2	PQ0663

30	12	23.5	7	2	S58797	serine/threonine-s
31	12	23.5	8	2	PA0035	protein QA300039 -
32	12	23.5	8	2	A35768	T-cell receptor al
33	12	23.5	8	2	PQ0701	unidentified 6.5/3
34	12	23.5	8	2	T48890	hypothetical prote
35	11	21.6	4	2	S47552	ubiquitin - rat
36	11	21.6	5	2	PT0525	T-cell receptor be
37	11	21.6	5	2	PT0700	T-cell receptor be
38	11	21.6	5	2	PT0608	T-cell receptor be
39	11	21.6	6	2	I51434	H4 histone - Afric
40	11	21.6	7	2	A34026	acetylcholinestera
41	11	21.6	7	2	PT0620	T-cell receptor be
42	11	21.6	7	2	PT0556	T-cell receptor be
43	11	21.6	7	2	PT0542	T-cell receptor be
44	11	21.6	7	2	PT0676	T-cell receptor be
45	11	21.6	7	2	PT0581	T-cell receptor be
46	11	21.6	7	2	PT0671	T-cell receptor be
47	11	21.6	7	4	S15597	orf 4 xara 5'-regi
48	11	21.6	8	2	PT0279	Ig heavy chain CRD
49	11	21.6	8	2	PT0522	T-cell receptor be
50	11	21.6	8	2	PT0547	T-cell receptor be
51	10	19.6	3	3	GKHU	growth-modulating
52	10	19.6	5	2	B31836	20K protein - Rick
53	10	19.6	5	2	F22565	R-phycocerythrin ga
54	10	19.6	5	2	T10954	hypothetical prote
55	10	19.6	6	2	JN0861	peptidyl-dipeptida
56	10	19.6	6	2	JU0355	lipopeptide WS1279
57	10	19.6	6	2	A11490	pyruvate kinase (E
58	10	19.6	7	2	S38516	mabulin II chain
59	10	19.6	7	2	S70335	endospore protein,
60	10	19.6	7	2	A12016	formylglycinamide
61	10	19.6	7	2	I46868	alpha-myosin heavy
62	10	19.6	7	4	I56695	hypothetical L2 pr
63	10	19.6	8	2	S63493	dissimilatory sulf
64	10	19.6	8	2	PC1002	leucine-tRNA ligas
65	10	19.6	8	2	A37521	R-phycocerythrin ga
66	10	19.6	8	2	A46306	spasmogenic toxin
67	10	19.6	8	2	B27867	homeotic protein U
68	10	19.6	8	2	A61467	penalbumin - Adeli
69	9	17.6	3	3	A22565	R-phycocerythrin al
70	9	17.6	4	2	I51049	metallothionein-A
71	9	17.6	4	2	S43959	Ig mu chain V regi
72	9	17.6	4	2	S55238	pallidipin - assas
73	9	17.6	5	2	A33882	cadmium-binding pe
74	9	17.6	5	2	B45525	actin I - malaria
75	9	17.6	5	2	S65726	hemoglobin, extrac
76	9	17.6	6	2	I37027	protamine P1 - gor
77	9	17.6	6	2	H48394	glycoprotein compo
78	9	17.6	6	2	I67345	MHC H2-K-k cell su
79	9	17.6	6	2	I65546	MHC H2-L antigen -
80	9	17.6	6	2	PT0652	T-cell receptor be
81	9	17.6	6	2	F41946	T-cell receptor ga
82	9	17.6	6	2	S71349	beta-crystallin B2
83	9	17.6	6	2	S29881	Na+/K+-exchanging
84	9	17.6	6	4	I79564	hypothetical TCU3
85	9	17.6	6	2	B33882	cadmium-binding he
86	9	17.6	7	2	PH1602	Ig H chain V-D-J r
87	9	17.6	7	2	PT0579	T-cell receptor be
88	9	17.6	7	2	A38671	peptidylglycine mo
89	9	17.6	7	2	PH0932	T-cell receptor be
90	9	17.6	7	2	A58512	venom heptapeptide
91	9	17.6	7	2	S08606	hypothetical prote
92	9	17.6	8	2	PH1407	Ig heavy chain V r
93	9	17.6	8	2	PH0803	T-cell receptor al
94	9	17.6	8	2	S19288	acylase - Kluyvera
95	9	17.6	8	2	A35180	neutral proteinase
96	8	15.7	3	3	RHSHT	thyloliberin - she
97	8	15.7	3	3	A92971	thyloliberin - eas
98	8	15.7	3	3	RHTDFO	thyloliberin - Bom
99	8	15.7	3	3	RHPGT	thyloliberin - pig
100	8	15.7	3	3	A60898	bursin - chicken

## ALIGNMENTS

## RESULT 1

PT0368  
 Ig gamma chain C region (gamma-1) - human (fragment)  
 C;Species: Homo sapiens (man)  
 C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 16-Aug-1996  
 C;Accession: PT0368  
 R;Milili, M.; Fougereau, M.; Guglielmi, P.; Schiff, C.  
 Mol. Immunol. 28, 753-761, 1991  
 A;Title: Early occurrence of immunoglobulin isotype switching in human fetal liver.  
 A;Reference number: PT0368; MUID:91312348; PMID:1906981  
 A;Accession: PT0368  
 A;Molecule type: mRNA  
 A;Residues: 1-8 <MIL>  
 A;Experimental source: fetal liver  
 C;Keywords: immunoglobulin

Query Match 37.3%; Score 19; DB 2; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LHRG 5  
 | | |  
 Db 1 LHQG 4

## RESULT 2

PH0934  
 T-cell receptor beta chain V-D-J region (clone 5) - rat (fragment)  
 C;Species: Rattus norvegicus (Norway rat)  
 C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
 C;Accession: PH0934  
 R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
 J. Exp. Med. 174, 1467-1476, 1991  
 A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
 A;Reference number: PH0891; MUID:92078857; PMID:1836012  
 A;Accession: PH0934  
 A;Molecule type: mRNA  
 A;Residues: 1-8 <GOL>  
 A;Experimental source: complete Freund's adjuvant-immunized lymph node  
 A;Note: the authors translated the codon CAG for residue 7 as Glu  
 C;Keywords: T-cell receptor

Query Match 35.3%; Score 18; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGN 6  
 | | |  
 Db 1 CASSGN 6

## RESULT 3

SI4159  
 parasporal crystal protein Cry7C - Bacillus thuringiensis (fragment)  
 N;Alternate names: delta-endotoxin  
 C;Species: Bacillus thuringiensis  
 C;Date: 19-Mar-1997 #sequence\_revision 18-Jul-1997 #text\_change 18-Jul-1997  
 C;Accession: SI4159  
 R;Convents, D.; Cherlet, M.; van Damme, J.; Lasters, I.; Lauwereys, M.  
 Eur. J. Biochem. 195, 631-635, 1991  
 A;Title: Two structural domains as a general fold of the toxic fragment of the Bacillus  
 A;Reference number: SI4087; MUID:91153300; PMID:1847865  
 A;Accession: SI4159  
 A;Molecule type: Protein  
 A;Residues: 1-6 <CON>

Query Match 31.4%; Score 16; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GNS 7  
 | | |  
 Db 4 GNS 6

## RESULT 4

B34818  
 vicillin 57K chain - pigeon pea (fragment)  
 C;Species: Cajanus cajan (pigeon pea)  
 C;Date: 13-Jul-1990 #sequence\_revision 13-Jul-1990 #text\_change 30-Sep-1993  
 C;Accession: B34818  
 R;Mawal, Y.R.; Mawal, M.R.; Ranjekar, P.K.  
 Biochem. Biophys. Res. Commun. 166, 1446-1452, 1990  
 A;Title: Unusual denaturation properties of vicillin from Cajanus cajan.  
 A;Reference number: A34818; MUID:90165956; PMID:2306256  
 A;Accession: B34818  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-7 <MAW>

Query Match 31.4%; Score 16; DB 2; Length 7;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRG 5  
 | | |  
 Db 3 CMESG 7

## RESULT 5

C61512  
 variant surface glycoprotein MITat 1.4 - Trypanosoma brucei (fragment)  
 C;Species: Trypanosoma brucei  
 C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
 C;Accession: C61512  
 R;Holder, A.A.; Cross, G.A.M.  
 Mol. Biochem. Parasitol. 2, 135-150, 1981  
 A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termir  
 A;Reference number: A61512; MUID:81172836; PMID:6163983  
 A;Accession: C61512  
 A;Molecule type: protein  
 A;Status: preliminary  
 A;Residues: 1-8 <HOL>  
 A;Cross-references: UNIPROT:Q7M3S3  
 C;Keywords: glycoprotein

Query Match 31.4%; Score 16; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 NSC 8  
 | | |  
 Db 4 NAC 6

## RESULT 6

D61512  
 variant surface glycoprotein MITat 1.6 - Trypanosoma brucei (fragment)  
 C;Species: Trypanosoma brucei  
 C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
 C;Accession: D61512  
 R;Holder, A.A.; Cross, G.A.M.  
 Mol. Biochem. Parasitol. 2, 135-150, 1981  
 A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termir  
 A;Reference number: A61512; MUID:81172836; PMID:6163983  
 A;Accession: D61512  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 A;Cross-references: UNIPROT:Q7M3S2  
 C;Keywords: glycoprotein

Query Match 31.4%; Score 16; DB 2; Length 8;

Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GNSC 8  
| : |  
Db 3 GETC 6

RESULT 7  
I55382  
hypothetical peptide PAlI promoter region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 20-Apr-2000  
C/Accession: I55382  
R/Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.  
J. Biol. Chem. 268, 10739-10745, 1993  
A/Title: The two allele sequences of a common polymorphism in the promoter of the plasmid  
A/Reference number: I55382; MUID:92266509; PMID:8388372  
A/Accession: I55382  
A/Status: translation not shown; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-7 <DAW>  
A/Cross-references: GB:M91557; NID:G150020; PIDN:AAA60110.1; PID:G150021  
C/Comment: This is the hypothetical translation of a sequence from the PAlI gene promoter  
C/Genetics:  
A/Gene: GDB:PAlI  
A/Cross-references: GDB:I20297; OMIM:173360  
A/Map position: 7q21.3-7q22

Query Match 29.4%; Score 15; DB 4; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RGNS 7  
| : |  
Db 3 RGES 6

RESULT 8  
A41946  
T-cell receptor gamma chain (1t.22) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C/Accession: A41946  
R/Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A/Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene  
A/Reference number: A41946; MUID:92049316; PMID:1658619  
A/Accession: A41946  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-6 <WHE>  
C/Keywords: T-cell receptor

Query Match 27.5%; Score 14; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HRGN 6  
| : |  
Db 1 YRGS 4

RESULT 9  
S45311  
microcin C7 - Escherichia coli plasmid pMccc7  
C/Species: Escherichia coli  
C/Date: 10-Dec-1994 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
C/Accession: S45311  
R/Gonzalez-Pastor, J.E.; San Millan, J.L.; Moreno, F.  
Nature 369, 281, 1994  
A/Title: The smallest known gene.  
A/Reference number: S45311; MUID:94239518; PMID:8183363

Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GNSC 8  
| : |  
Db 3 GETC 6

RESULT 7  
I55382  
hypothetical peptide PAlI promoter region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 20-Apr-2000  
C/Accession: I55382  
R/Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.  
J. Biol. Chem. 268, 10739-10745, 1993  
A/Title: The two allele sequences of a common polymorphism in the promoter of the plasmid  
A/Reference number: I55382; MUID:92266509; PMID:8388372  
A/Accession: I55382  
A/Status: translation not shown; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-7 <DAW>  
A/Cross-references: GB:M91557; NID:G150020; PIDN:AAA60110.1; PID:G150021  
C/Comment: This is the hypothetical translation of a sequence from the PAlI gene promoter  
C/Genetics:  
A/Gene: GDB:PAlI  
A/Cross-references: GDB:I20297; OMIM:173360  
A/Map position: 7q21.3-7q22

Query Match 29.4%; Score 15; DB 4; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RGNS 7  
| : |  
Db 3 RGES 6

RESULT 8  
A41946  
T-cell receptor gamma chain (1t.22) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C/Accession: A41946  
R/Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A/Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene  
A/Reference number: A41946; MUID:92049316; PMID:1658619  
A/Accession: A41946  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-6 <WHE>  
C/Keywords: T-cell receptor

Query Match 27.5%; Score 14; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HRGN 6  
| : |  
Db 1 YRGS 4

RESULT 9  
S45311  
microcin C7 - Escherichia coli plasmid pMccc7  
C/Species: Escherichia coli  
C/Date: 10-Dec-1994 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
C/Accession: S45311  
R/Gonzalez-Pastor, J.E.; San Millan, J.L.; Moreno, F.  
Nature 369, 281, 1994  
A/Title: The smallest known gene.  
A/Reference number: S45311; MUID:94239518; PMID:8183363

Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GNSC 8  
| : |  
Db 3 GETC 6

RESULT 7  
I55382  
hypothetical peptide PAlI promoter region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 20-Apr-2000  
C/Accession: I55382  
R/Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.  
J. Biol. Chem. 268, 10739-10745, 1993  
A/Title: The two allele sequences of a common polymorphism in the promoter of the plasmid  
A/Reference number: I55382; MUID:92266509; PMID:8388372  
A/Accession: I55382  
A/Status: translation not shown; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-7 <DAW>  
A/Cross-references: GB:M91557; NID:G150020; PIDN:AAA60110.1; PID:G150021  
C/Comment: This is the hypothetical translation of a sequence from the PAlI gene promoter  
C/Genetics:  
A/Gene: GDB:PAlI  
A/Cross-references: GDB:I20297; OMIM:173360  
A/Map position: 7q21.3-7q22

Query Match 29.4%; Score 15; DB 4; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RGNS 7  
| : |  
Db 3 RGES 6

RESULT 8  
A41946  
T-cell receptor gamma chain (1t.22) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C/Accession: A41946  
R/Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A/Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene  
A/Reference number: A41946; MUID:92049316; PMID:1658619  
A/Accession: A41946  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-6 <WHE>  
C/Keywords: T-cell receptor

Query Match 27.5%; Score 14; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HRGN 6  
| : |  
Db 1 YRGS 4

RESULT 9  
S45311  
microcin C7 - Escherichia coli plasmid pMccc7  
C/Species: Escherichia coli  
C/Date: 10-Dec-1994 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
C/Accession: S45311  
R/Gonzalez-Pastor, J.E.; San Millan, J.L.; Moreno, F.  
Nature 369, 281, 1994  
A/Title: The smallest known gene.  
A/Reference number: S45311; MUID:94239518; PMID:8183363

Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GNSC 8  
| : |  
Db 3 GETC 6

RESULT 7  
I55382  
hypothetical peptide PAlI promoter region - human (fragment)  
C/Species: Homo sapiens (man)  
C/Date: 16-Apr-1999 #sequence\_revision 16-Apr-1999 #text\_change 20-Apr-2000  
C/Accession: I55382  
R/Dawson, S.J.; Wiman, B.; Hamsten, A.; Green, F.; Humphries, S.; Henney, A.M.  
J. Biol. Chem. 268, 10739-10745, 1993  
A/Title: The two allele sequences of a common polymorphism in the promoter of the plasmid  
A/Reference number: I55382; MUID:92266509; PMID:8388372  
A/Accession: I55382  
A/Status: translation not shown; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-7 <DAW>  
A/Cross-references: GB:M91557; NID:G150020; PIDN:AAA60110.1; PID:G150021  
C/Comment: This is the hypothetical translation of a sequence from the PAlI gene promoter  
C/Genetics:  
A/Gene: GDB:PAlI  
A/Cross-references: GDB:I20297; OMIM:173360  
A/Map position: 7q21.3-7q22

Query Match 29.4%; Score 15; DB 4; Length 7;  
Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RGNS 7  
| : |  
Db 3 RGES 6

RESULT 8  
A41946  
T-cell receptor gamma chain (1t.22) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C/Accession: A41946  
R/Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991  
A/Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma gene  
A/Reference number: A41946; MUID:92049316; PMID:1658619  
A/Accession: A41946  
A/Status: preliminary; not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-6 <WHE>  
C/Keywords: T-cell receptor

Query Match 27.5%; Score 14; DB 2; Length 6;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 3 HRGN 6  
| : |  
Db 1 YRGS 4

RESULT 9  
S45311  
microcin C7 - Escherichia coli plasmid pMccc7  
C/Species: Escherichia coli  
C/Date: 10-Dec-1994 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
C/Accession: S45311  
R/Gonzalez-Pastor, J.E.; San Millan, J.L.; Moreno, F.  
Nature 369, 281, 1994  
A/Title: The smallest known gene.  
A/Reference number: S45311; MUID:94239518; PMID:8183363

A/Accession: S45311  
A/Status: not compared with conceptual translation  
A/Molecule type: DNA  
A/Residues: 1-7 <GON>  
A/Cross-references: UNIPROT:Q47505  
C/Genetics:  
A/Gene: mcca  
A/Genome: plasmid pMccc7  
C/Keywords: antibacterial  
F/1/Modified site: N-formylmethionine #status predicted  
F/7/Modified site: asparagine derivative (Asn) #status experimental

Query Match 27.5%; Score 14; DB 2; Length 7;  
Best Local Similarity 33.3%; Pred. No. 2.8e+05;  
Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 LHRGNS 7  
| : |  
Db 1 MRTGNA 6

RESULT 10  
S59622  
metallothionein isoform a, cadmium-binding - Ariantha arbustorum (terrestrial snail) (frag  
C/Species: Ariantha arbustorum  
C/Date: 19-Mar-1997 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
C/Accession: S59622  
R/Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.  
Biochem. J. 311, 951-957, 1995  
A/Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothione  
A/Reference number: S59621; MUID:96067616; PMID:7487956  
A/Accession: S59622  
A/Molecule type: protein  
A/Residues: 1-8 <BER>  
A/Cross-references: UNIPROT:P55946  
C/Superfamily: metallothionein  
C/Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 27.5%; Score 14; DB 2; Length 8;  
Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 NSC 8  
| : |  
Db 3 SSC 5

RESULT 11  
PH1618  
Ig H chain V-D-J region (clone B-less 33) - mouse (fragment)  
C/Species: Mus musculus (house mouse)  
C/Date: 02-Jun-1994 #sequence\_revision 02-Jun-1994 #text\_change 17-Mar-1999  
C/Accession: PH1618  
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.  
J. Exp. Med. 178, 317-329, 1993  
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice  
A/Reference number: PH1580; MUID:93301609; PMID:8315387  
A/Accession: PH1618  
A/Molecule type: DNA  
A/Residues: 1-8 <LEV>  
A/Experimental source: bone marrow pre-B lymphocyte  
C/Keywords: immunoglobulin

Query Match 27.5%; Score 14; DB 2; Length 8;  
Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRG 5  
| : |  
Db 1 CARHG 5

RESULT 12

A25836  
 L-serine ammonia-lyase (EC 4.3.1.17) - Escherichia coli (fragment)  
 C;Species: Escherichia coli  
 C;Date: 24-Jan-1988 #sequence\_revision 24-Jan-1988 #text\_change 09-Jul-2004  
 R;Accession: A25836  
 R;Heincz, M.C.; McFall, E.  
 J. Bacteriol. 123, 1163-1168, 1975  
 A;Title: N-terminal amino acid sequences of D-serine deaminases of wild-type and operated  
 A;Reference number: A25836; MUID:76005414; PMID:1099073  
 A;Contents: K12  
 A;Accession: A25836  
 A;Molecule type: protein  
 A;Residues: 1-8 <HEI>  
 A;Cross-references: UNIPROT:Q7M194  
 C;Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase; serine

Query Match 27.5%; Score 14; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;  
 QY 5 GNSC 8  
 DB 5 GRHC 8

RESULT 13  
 XGHUEU  
 urine glycopeptide - human  
 C;Species: Homo sapiens (man)  
 C;Date: 20-Jun-2000 #sequence\_revision 20-Jun-2000 #text\_change 16-Aug-2004  
 C;Accession: A03188  
 R;Lote, C.J.; Weiss, J.B.  
 Biochem. J. 123, 25P, 1971  
 A;Title: Identification in urine of a low-molecular-weight polar glycopeptide containing  
 A;Reference number: A03188; MUID:72062338; PMID:5126885  
 A;Accession: A03188  
 A;Molecule type: protein  
 A;Residues: 1-8 <LOT>  
 A;Cross-references: UNIPROT:P02729  
 C;Comment: The identity of the glycoprotein from which this peptide is derived is unknown  
 re has also been found (see PIR:XGHUEU).  
 C;Keywords: glycoprotein  
 F;1/Binding site: carbohydrate (Cys) (covalent) #status experimental

Query Match 27.5%; Score 14; DB 2; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CLH 3  
 DB 1 CEH 3

RESULT 14  
 B22565  
 R-phycoerythrin alpha-2 chain - red alga (Gastroclonium coulteri) (fragment)  
 C;Species: Gastroclonium coulteri  
 C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
 C;Accession: B22565  
 R;Klotz, A.V.; Glazer, A.N.  
 J. Biol. Chem. 260, 4856-4863, 1985  
 A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
 A;Reference number: A22565; MUID:85182601; PMID:3886644  
 A;Accession: B22565  
 A;Molecule type: protein  
 A;Residues: 1-5 <KLO>

Query Match 25.5%; Score 13; DB 2; Length 5;  
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 1 CLHR 4  
 DB 1

Db 2 CVPR 5

RESULT 15  
 C22565  
 R-phycoerythrin beta-1 chain - red alga (Gastroclonium coulteri) (fragment)  
 C;Species: Gastroclonium coulteri  
 C;Date: 07-Mar-1988 #sequence\_revision 07-Mar-1988 #text\_change 23-Mar-1993  
 C;Accession: C22565  
 R;Klotz, A.V.; Glazer, A.N.  
 J. Biol. Chem. 260, 4856-4863, 1985  
 A;Title: Characterization of the bilin attachment sites in R-phycoerythrin.  
 A;Reference number: A22565; MUID:85182601; PMID:3886644  
 A;Accession: C22565  
 A;Molecule type: protein  
 A;Residues: 1-6 <KLO>

Query Match 25.5%; Score 13; DB 2; Length 6;  
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CL 2  
 DB 4 CL 5

Search completed: August 3, 2005, 12:20:25  
 Job time : 39 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:03:27 ; Search time 171 Seconds  
(without alignments)  
23.957 Million cell updates/sec

Title: US-09-910-582B-9  
Perfect score: 51  
Sequence: 1 CLHRGNSC 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 790

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : UniProt\_03.\*

1: uniprot\_sprot.\*  
2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	23	45.1	8	2	Q6xw6 anthreptes
2	20	39.2	8	2	Q6h0c6 isoetes fla
3	17	33.3	8	2	Q37854 bacterioph
4	16	31.4	7	2	Q66113 cherry leaf
5	16	31.4	8	2	Q7m382 trypanosoma
6	16	31.4	8	2	Q7m383 trypanosoma
7	15	29.4	7	2	Q67113 influenza a
8	15	29.4	8	2	Q28866 megaptera n
9	14	27.5	7	2	Q47505 escherichia
10	14	27.5	8	1	GLUR_HUMAN
11	14	27.5	8	2	Q7m194 escherichia
12	13	25.5	5	1	TPIS CANFA
13	13	25.5	7	1	TY51_LITRU
14	13	25.5	7	2	Q42564 fugu rubrip
15	13	25.5	8	1	COXG_RAT
16	13	25.5	8	2	Q15890 homo sapien
17	13	25.5	8	2	Q9Y4X6 homo sapien
18	13	25.5	8	2	O02831 cryctolagus
19	13	25.5	8	2	Q7m1f1 raphanus sa
20	13	25.5	8	2	Q7m056 mus sp. gen
21	13	25.5	8	2	Q80WD5 mus spretus
22	13	25.5	8	2	Q80WD6 mus musculus
23	13	25.5	8	2	Q84156 orf virus.
24	12	23.5	6	1	FARP MONEX
25	12	23.5	6	1	TMOF_SARBU
26	12	23.5	7	2	UN06_PINPS
27	12	23.5	8	1	Q66205 transmissib
28	12	23.5	8	1	CLIP_THICU
29	12	23.5	8	2	Q15889 homo sapien
30	12	23.5	8	2	Q7Z6G0 homo sapien
31	12	23.5	8	2	Q8MUN6 heliconius

#### ALIGNMENTS

32	12	23.5	8	2	Q9GD00	Q9gd00 masoala mad
33	12	23.5	8	2	Q699J0	Q699j0 beta vulgar
34	12	23.5	8	2	Q6ZZ01	Q6zz01 silene con
35	12	23.5	8	2	Q6ZZ02	Q6zz02 lychnis cor
36	12	23.5	8	2	Q7MIU0	Q7miu0 oryza sativ
37	12	23.5	8	2	Q9JLD7	Q9jld7 mesocricetu
38	12	23.5	8	2	Q7ZPJ1	Q7zpj1 human immun
39	11	21.6	5	1	UXA4_CHLTR	F38005 chlamydia t
40	11	21.6	7	1	UF04_MOUSE	R38642 mus musculus
41	11	21.6	7	2	Q8GLI2	Q8gli2 borrelia bu
42	11	21.6	7	2	Q63480	Q63480 rattus norv
43	11	21.6	8	1	ALL5_CYDPO	R82156 cydia pomon
44	11	21.6	8	2	Q15888	Q15888 homo sapien
45	11	21.6	8	2	Q69YH8	Q69yh8 homo sapien
46	11	21.6	8	2	Q9UHK1	Q9uhk1 homo sapien
47	11	21.6	8	2	Q7RBP6	Q7rbp6 plasmodium
48	11	21.6	8	2	Q9AVA0	Q9ava0 varanus sem
49	11	21.6	8	2	Q6YLT8	Q6ylt8 sciadopitys
50	11	21.6	8	2	Q7OY68	Q7oy68 prostanther
51	11	21.6	8	2	Q7OY69	Q7oy69 syncolostem
52	11	21.6	8	2	Q7OY84	Q7oy84 plectranthu
53	11	21.6	8	2	Q32560	Q32560 escherichia
54	11	21.6	8	2	P83531	P83531 lactobacill
55	11	21.6	8	2	Q56429	Q56429 thermus the
56	11	21.6	8	2	Q79AG6	Q79ag6 pantoea agg
57	11	21.6	8	2	Q7T863	Q7t863 largemouth
58	10	19.6	3	1	GRWM_HUMAN	P01157 homo sapien
59	10	19.6	5	1	AP21_EISFO	P84182 eisenia foe
60	10	19.6	7	2	Q28742	Q28742 cryctolagus
61	10	19.6	7	2	Q9CSB3	Q9csb3 arabidopsis
62	10	19.6	7	2	P72081	P72081 nocardia la
63	10	19.6	8	1	ANG2_BOTJA	Q10582 bothrops ja
64	10	19.6	8	1	COM2_CONPU	P58785 conus purpu
65	10	19.6	8	1	LCK1_LEUMA	P21140 leucophaea
66	10	19.6	8	1	LCK3_LEUMA	P21142 leucophaea
67	10	19.6	8	1	PK1_PERAM	P82685 periplaneta
68	10	19.6	8	1	PK3_PERAM	P82687 periplaneta
69	10	19.6	8	1	PK5_PERAM	P82689 periplaneta
70	10	19.6	8	1	TXVI_PHONI	Q7m3p1 phoneutraia
71	10	19.6	8	2	Q05403	Q05403 saccharomyc
72	10	19.6	8	2	Q16468	Q16468 homo sapien
73	10	19.6	8	2	Q81V87	Q81v87 homo sapien
74	10	19.6	8	2	Q6LD47	Q6ld47 homo sapien
75	10	19.6	8	2	Q7Z4N9	Q7z4n9 homo sapien
76	10	19.6	8	2	Q9BYV5	Q9byv5 homo sapien
77	10	19.6	8	2	Q7RC74	Q7rc74 plasmodium
78	10	19.6	8	2	Q9BF82	Q9bf82 ursus arcto
79	10	19.6	8	2	Q9BF83	Q9bf83 canis fami
80	10	19.6	8	2	Q9BF84	Q9bf84 panthera on
81	10	19.6	8	2	Q9BF85	Q9bf85 leopardus p
82	10	19.6	8	2	Q9BF86	Q9bf86 felis silve
83	10	19.6	8	2	Q9BF87	Q9bf87 tapirus ind
84	10	19.6	8	2	Q9BF88	Q9bf88 equus cabal
85	10	19.6	8	2	Q9BF89	Q9bf89 okapia john
86	10	19.6	8	2	Q9BF90	Q9bf90 tragelaphus
87	10	19.6	8	2	Q9BF91	Q9bf91 hippopotamu
88	10	19.6	8	2	Q9BF94	Q9bf94 nycteris th
89	10	19.6	8	2	Q9BF95	Q9bf95 roussettus l
90	10	19.6	8	2	Q9BF96	Q9bf96 pteropus gi
91	10	19.6	8	2	Q9BF97	Q9bf97 artibeus ja
92	10	19.6	8	2	Q9BF98	Q9bf98 callimico g
93	10	19.6	8	2	Q9BF99	Q9bf99 hylobates c
94	10	19.6	8	2	Q9BFA0	Q9bfa0 macaca mula
95	10	19.6	8	2	Q9BFA1	Q9bfa1 ateles fusc
96	10	19.6	8	2	Q9BFA2	Q9bfa2 tarsius ban
97	10	19.6	8	2	Q9BFA3	Q9bfa3 lemur catta
98	10	19.6	8	2	Q9BFA4	Q9bfa4 tupiaa mino
99	10	19.6	8	2	Q9BFA5	Q9bfa5 cynocephalu
100	10	19.6	8	2	Q9BFA6	Q9bfa6 crycteropus

```

RESULT 1
Q6XFW6 ID Q6XFW6 PRELIMINARY; PRT; 8 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome oxidase III (Fragment).
GN Name=COX3;
OS Anthreptes collaris (collared sunbird).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Passeriformes; Passeroidea;
OC Nectariniidae; Anthreptes.
OX NCBI_TaxID=208075;
RN [1]
RN SEQUENCE FROM N.A.
RA Bowie R.C.K., Hackett S.J., Fjeldsaa J., Crowe T.M.;
RL Submitted (FEB-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY234003; AAF69784.1; -.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON TER 8
SQ SEQUENCE 8 AA; 884 MW; F7A5B1EDC6D1EDD6 CRC64;

Query Match 45.1%; Score 23; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 HRGNSC 8
DB 3 HQHSC 8

RESULT 2
Q6HOC6 ID Q6HOC6 PRELIMINARY; PRT; 8 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leafy (Fragment).
OS Isoetes flaccida.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Lycopodiophyta; Isoetopsida; Isoetales; Isoetaceae; Isoetes.
OX NCBI_TaxID=49763;
RN [1]
RN SEQUENCE FROM N.A.
RA Hoot S.B., Napier N.S., Taylor W.Carl.;
RT "Revealing unknown or extinct lineages within Isoetes (Isoetaceae)
RT using DNA sequences from hybrids.";
RL Am. J. Bot. 91:899-904(2004).
DR EMBL; AY541784; AAS79402.1; -.
FT NON TER 1
FT NON TER 8
SQ SEQUENCE 8 AA; 918 MW; 3921B76EB33B1864 CRC64;

Query Match 39.2%; Score 20; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RGNSC 8
DB 1 RGEKC 5

RESULT 3
Q37854 ID Q37854 PRELIMINARY; PRT; 8 AA.
AC Q37854;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE Variant surface glycoprotein Mitat 1.6 (Fragment).

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DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Coliphage gene of unknown function, 5'end. (Fragment).
OS Bacteriophage R17.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus.
OX NCBI_TaxID=12026;
RN [1]
RN SEQUENCE FROM N.A.
RX MEDLINE=73224987; PubMed=4352721;
RA Rensing U.F.E.;
RT "A sequence of seventy-three nucleotides from the coliphage R17
RT genome.";
RL Biochem. J. 131:593-604(1973).
DR EMBL; M24820; AAA72755.1; -.
FT NON TER 8
SQ SEQUENCE 8 AA; 969 MW; ECB45412C1E72726 CRC64;

Query Match 33.3%; Score 17; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 LHRGNS 7
DB 3 LHVRNS 8

RESULT 4
Q66113 ID Q66113 PRELIMINARY; PRT; 7 AA.
AC Q66113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE C-terminus of the viral replicase (Fragment).
OS Cherry leaf roll virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Comoviridae;
OC Nepovirus; Subgroup C.
OX NCBI_TaxID=12615;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=Walnut;
RX MEDLINE=96124520; PubMed=8560786;
RA Borja M., Sanchez F., Rowhani A., Bruening G., Ponz F.;
RT "Long, nearly identical untranslated sequences at the 3' terminal
RT regions of the genomic RNAs of cherry leafroll virus (walnut
RT strain).";
RL Virus Genes 10:245-252(1995).
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN=Walnut;
RA Borja M.;
RL Thesis (1992), Biologia Molecular y Virologia Vegetal, CIT-INIA.
DR EMBL; Z34265; CAA84019.1; -.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 7 AA; 800 MW; 7417672EBDC6D740 CRC64;

Query Match 31.4%; Score 16; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLHR 4
DB 4 CLPR 7

RESULT 5
Q7M3S2 ID Q7M3S2 PRELIMINARY; PRT; 8 AA.
AC Q7M3S2;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Variant surface glycoprotein Mitat 1.6 (Fragment).

```

```

OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE
RX MEDLINE=81172836; PubMed=6163983; DOI=10.1016/0166-6851(81)90095-5;
RA Holder A.A., Cross G.A.M.;
RT "Glycopeptides from variant surface glycoproteins of Trypanosoma
RT brucei. C-terminal location of antigenically cross-reacting
RT carbohydrate moieties.";
RL Mol. Biochem. Parasitol. 2:135-150(1981).
DR PIR; D61512; D61512. 1
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 967 MW; 74033BEA1AB187B03 CRC64;

Query Match 31.4%; Score 16; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GNSC 8
DB 3 GETC 6

RESULT 6
Q7M3S3
ID Q7M3S3 PRELIMINARY; PRT; 8 AA.
AC Q7M3S3; 2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Variant surface glycoprotein MITat 1.4 (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE.
RX MEDLINE=81172836; PubMed=6163983; DOI=10.1016/0166-6851(81)90095-5;
RA Holder A.A., Cross G.A.M.;
RT "Glycopeptides from variant surface glycoproteins of Trypanosoma
RT brucei. C-terminal location of antigenically cross-reacting
RT carbohydrate moieties.";
RL Mol. Biochem. Parasitol. 2:135-150(1981).
DR PIR; C61512; C61512. 1
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 979 MW; 74033BEA1AB187B03 CRC64;

Query Match 31.4%; Score 16; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 NSC 8
DB 4 NAC 6

RESULT 7
Q67113
ID Q67113 PRELIMINARY; PRT; 7 AA.
AC Q67113;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Influenza virus type A (Udorn/72) hemagglutinin (seg 4) cDNA, 3' end.
DE (Fragment).
OS Influenza A virus.
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=11320;
RN [1]
RP SEQUENCE FROM N.A.

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RX MEDLINE=81001892; PubMed=7407922; DOI=10.1016/0092-8674(80)90486-9;
RA Dhar R., Chanock R.M., Lai C.-J.;
RT "Nonviral oligonucleotides at the 5' terminus of cytoplasmic influenza
RT viral mRNA deduced from cloned complete genomic sequences.";
RL Cell 21:495-500(1980).
DR EMBL; M25045; AAA43202.1; -.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 7 AA; 834 MW; 605EB0544EA40030 CRC64;

Query Match 29.4%; Score 15; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 1.6e+06;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RGNSC 8
DB 2 RCNIC 6

RESULT 8
Q28866
ID Q28866 PRELIMINARY; PRT; 8 AA.
AC Q28866;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-MAY-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Actin protein (Fragment).
GN Name=actin;
OS Megaptera novaeangliae (Humpback whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Mysticeti;
OC Balanopteridae; Megaptera.
OX NCBI_TaxID=9773;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94285813; PubMed=7912407;
RA Palumbi S.R., Baker C.S.;
RT "Contrasting population structure from nuclear intron sequences and
RT mtDNA of humpback whales.";
RL Mol. Biol. Evol. 11:426-435(1994).
DR EMBL; S73467; AAD14118.1; -.
FT NON_TER 8
FT NON_TER 8
SQ SEQUENCE 8 AA; 906 MW; 69C866D1F4177408 CRC64;

Query Match 29.4%; Score 15; DB 2; Length 8;
Best Local Similarity 66.7%; Pred. No. 1.6e+06;
Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 HRG 5
DB 5 HQG 7

RESULT 9
Q47505
ID Q47505 PRELIMINARY; PRT; 7 AA.
AC Q47505;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE MccA protein.
DE Name=mccA;
GN Escherichia coli.
OS Escherichia coli.
OG Plasmid pMccC7.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96099297; PubMed=8522520;
RA Gonzalez-Pastor J.E., San Millan J.L., Castilla M.A., Moreno F.;
RT "Structure and organization of plasmid genes required to produce the
RT translation inhibitor microcin C7.";
RL J. Bacteriol. 177:7131-7140(1995).

```

RN [2]  
 RP SEQUENCE FROM N.A.  
 RA San Millan J.L.;  
 RL Submitted (FEB-1991) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; X57583; CAA40808.1; -.  
 DR PIR; S45311; S45311.  
 KW plasmid.  
 SQ SEQUENCE 7 AA; 763 MW; 644DD44861B406F0 CRC64;

Query Match 27.5%; Score 14; DB 2; Length 7;  
 Best Local Similarity 33.3%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 LHGNS 7  
 : ||:  
 Db 1 MRTGNA 6

## RESULT 10

GLUR\_HUMAN STANDARD; PRT; 8 AA.  
 AC P02729;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 21-JUL-1986 (Rel. 01, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Urine glycopeptide.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=72062338; PubMed=5126885;  
 RA Lote C.J., Weiss J.B.;  
 RT "Identification in urine of a low-molecular-weight highly polar  
 RT glycopeptide containing cysteinyl-galactose.";  
 RL Biochem J. 123:25P-25P(1971).  
 CC -1- FUNCTION: The identity of the glycoprotein from which this peptide  
 CC is derived is unknown. No physiological function has been  
 CC attributed. An erythrocyte membrane glycopeptide having a similar  
 CC structure has also been found.  
 CC PIR; A03188; XGHUEU.  
 DR GO; GO:0005576; C:extracellular; NAS.  
 KW Direct protein sequencing; Glycoprotein.  
 FT CARBOHYD 1 1 S-linked (Gal. . .).  
 SQ SEQUENCE 8 AA; 855 MW; C2D87AAIP5B1EB1E CRC64;

Query Match 27.5%; Score 14; DB 1; Length 8;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 CLH 3  
 : ||:  
 Db 1 CEH 3

## RESULT 11

Q7M194 PRELIMINARY; PRT; 8 AA.  
 AC Q7M194;  
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE L-serine ammonia-lyase (EC 4.3.1.17) (Fragment).  
 OS Escherichia coli.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
 OC Enterobacteriaceae; Escherichia.  
 OX NCBI\_TaxID=562;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=76005414; PubMed=1099073;  
 RA Heinicz M.C., McFall E.;  
 RT "N-terminal amino acid sequences of D-serine deaminases of wild-type

RT and operator-constitutive strains of Escherichia coli K-12.";  
 RL J. Bacteriol. 123:1163-1168(1975).  
 DR PIR; A25836; A25836.  
 DR GO; GO:0003941; F:L-serine ammonia-lyase activity; IEA.  
 FT NON\_TER 8  
 SQ SEQUENCE 8 AA; 906 MW; F7B1F40865BB05B6 CRC64;

Query Match 27.5%; Score 14; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GNSC 8  
 : ||:  
 Db 5 GRHC 8

## RESULT 12

TPIS\_CANFA STANDARD; PRT; 5 AA.  
 AC P54714;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Triosephosphate isomerase (EC 5.3.1.1) (TIM) (Triose-phosphate  
 DE isomerase) (Fragment).  
 GN Name-TPil;  
 OS Canis familiaris (Dog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.  
 OX NCBI\_TaxID=9615;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=98163340; PubMed=9504812;  
 RA Dunn M.J., Corbett J.M., Wheeler C.H.;  
 RT "HSC-2DPAGE and the two-dimensional gel electrophoresis database of  
 RT dog heart proteins.";  
 RL Electrophoresis 18:2795-2802(1997).  
 CC -1- CATALYTIC ACTIVITY: D-glyceraldehyde 3-phosphate = glycerone  
 CC phosphate.  
 CC -1- PATHWAY: Plays an important role in several metabolic pathways.  
 CC -1- SUBUNIT: Homodimer (By similarity).  
 CC -1- SIMILARITY: Belongs to the triosephosphate isomerase family.  
 DR HSC-2DPAGE; P54714; DOG.  
 DR InterPro; IPR000652; Triophos\_ismrse.  
 DR PROSITE; PS00171; TIM; PARTIAL.  
 KW Direct protein sequencing; Fatty acid biosynthesis; Gluconeogenesis;  
 KW Glycolysis; Isomerase; Pentose shunt.  
 FT NON\_TER 1 1  
 FT NON\_TER 5 5  
 SQ SEQUENCE 5 AA; 550 MW; 64444862C9A00000 CRC64;

Query Match 25.5%; Score 13; DB 1; Length 5;  
 Best Local Similarity 66.7%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 GNS 7  
 : ||:  
 Db 3 GNN 5

## RESULT 13

TV51\_LITRU STANDARD; PRT; 7 AA.  
 AC P82065;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Trypophyllin S.1.  
 OS Litoria rubella (Desert tree frog).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;  
 OC Pelodyadinae; Litoria.



OX NCBI\_TaxID=104895;  
 RN [1]  
 RP SEQUENCE, AND MASS SPECTROMETRY.  
 RC TISSUE=Skin secretion;  
 RA Steinborner S.T., Wabnitz P.A., Waugh R.J., Bowie J.H., Gao C.,  
 RA Tyler M.J., Wallace J.C.;  
 RT "The structure of new peptides from the Australian red tree frog  
 RT 'Litoria rubella'. The skin peptide profile as a probe for the study  
 RT of evolutionary trends of amphibians.";  
 RL Aust. J. Chem. 49:955-963(1996).  
 CC -1- FUNCTION: May act as a neuromodulator or neurotransmitter.  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- TISSUE SPECIFICITY: Expressed by the skin dorsal glands.  
 CC -1- MASS SPECTROMETRY: MW=965; METHOD=FAB; RANGE=1-7; NOTE=Ref.1.  
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;  
 KW Neuropeptide; Pyrrolidone carboxylic acid.  
 FT MOD\_RES 1 1 Pyrrolidone carboxylic acid.  
 FT MOD\_RES 7 7 Arginine amide.  
 FT MOD\_RES 9 9 Arginine amide.  
 SQ SEQUENCE 7 AA; 983 MW; 7401E9D3676046B0 CRC64;  
  
 Query Match 25.5%; Score 13; DB 1; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 3 HR 4  
 Db 6 HR 7  
  
 RESULT 14  
 ID 042564 PRELIMINARY; PRT; 7 AA.  
 AC 042564;  
 DT 01-JAN-1998 (TrEMBLrel. 05, Created)  
 DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
 DE Truncated voltage-gated sodium channel alpha subunit (Fragment).  
 GN Name=Scn8a;  
 OS Fugu rubripes (Japanese pufferfish) (Takifugu rubripes).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
 OC Tetraodontidae; Tetraodontinae; Tetraodontinae; Tetraodontinae;  
 OX NCBI\_TaxID=31033;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97442476; PubMed=9295353; DOI=10.1074/jbc.272.38.24008;  
 RA Plummer N.W., McBurney M.W., Meisler M.H.;  
 RT "Alternative splicing of the sodium channel SCN8A predicts a truncated  
 RT two-domain protein in fetal brain and non-neuronal cells.";  
 RL J. Biol. Chem. 272:24008-24015(1997).  
 DR EMBL; U97673; AAB80916.1;  
 DR GO; GO:0005216; F:ion channel activity; IEA.  
 KW Ionic channel.  
 FT NON\_TER 1 1  
 FT NON\_TER 7 7  
 SQ SEQUENCE 7 AA; 730 MW; 75B72EA2C73772A0 CRC64;  
  
 Query Match 25.5%; Score 13; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 1 CL 2  
 Db 5 CL 6,  
  
 RESULT 15  
 COXG\_RAT  
 ID COXG\_RAT STANDARD; PRT; 8 AA.  
 AC P80430;  
 DT 01-NOV-1995 (Rel. 32, Created)  
 DT 01-NOV-1995 (Rel. 32, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Cytochrome c oxidase polypeptide Vlb (EC 1.9.3.1) (Cytochrome c  
 DE oxidase subunit AED) (Fragment).  
 GN Name=Cox6b1; Synonyms=Cox6b;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE.  
 RC STRAIN=Wistar; TISSUE=Liver;  
 RX MEDLINE=95324529; PubMed=7601105;  
 RA Schaeffer H., Noack H., Halangk W., Brandt U., von Jagow G.;  
 RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and  
 RT amino-terminal sequences suggest identity of the fetal heart and the  
 RT adult liver isoform.";  
 RL Eur. J. Biochem. 230:235-241(1995).  
 CC -1- FUNCTION: This protein is one of the nuclear-coded polypeptide  
 CC chains of cytochrome c oxidase, the terminal oxidase in  
 CC mitochondrial electron transport. This protein may be one of the  
 CC heme-binding subunits of the oxidase.  
 CC -1- CATALYTIC ACTIVITY: 4 ferrocytochrome c + O(2) = 4 ferricytochrome  
 CC c + 2 H(2)O.  
 CC -1- SIMILARITY: Belongs to the cytochrome c oxidase Vlb family.  
 DR PIR; S65381; S65381.  
 KW Direct protein sequencing; Mitochondrion; Oxidoreductase.  
 FT NON\_TER 1 1  
 FT NON\_TER 8 8  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 1039 MW; 8101E9CAA73AE456 CRC64;  
  
 Query Match 25.5%; Score 13; DB 1; Length 8;  
 Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
 Matches 2; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
 Qy 3 HR 4  
 Db 7 HR 8  
  
 Search completed: August 3, 2005, 12:19:42  
 Job time : 173 secs

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GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 11:58:21 ; Search time 159 Seconds  
(without alignments)  
19.460 Million cell updates/sec

Title: US-09-910-582B-9  
Perfect score: 51  
Sequence: 1 CLHRGNSC 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 160390

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	51	100.0	8	4	AAB30898 Peptide w
2	51	100.0	8	4	AAB59303 Heart hom
3	31	60.8	8	3	AAV63252 Protocadh
4	30	58.8	8	2	AAV48836 Membrane
5	30	58.8	8	3	AAV61138 Cadherin-
6	30	58.8	8	5	ABG35010 Endostati
7	30	58.8	8	5	ABJ04479 HUVEC cel
8	29	56.9	8	2	AAV48662 Membrane
9	28	54.9	8	2	AAV48879 Membrane
10	28	54.9	8	5	ABB98083 FC effect
11	28	54.9	8	5	ABB98084 FC effect
12	27	52.9	8	5	ABJ04391 HUVEC cel
13	27	52.9	8	5	ABB98080 FC effect
14	26	51.0	7	2	AAW54868 Homo sapi
15	26	51.0	8	2	AAV96348 RGD cycli
16	26	51.0	8	2	AAW13414 Brain hom
17	26	51.0	8	3	AAAB17981 MMP inhib
18	26	51.0	8	3	AAV63634 Desmoglei
19	26	51.0	8	3	AAV07390 Brain hom
20	26	51.0	8	4	AAE11796 Phage pep
21	26	51.0	8	5	ABG35024 Endostati
22	26	51.0	8	5	ABG34980 Human pro
23	26	51.0	8	5	ABBA45686 Desmoglei
24	26	51.0	8	5	AAU10707 Brain hom
25	26	51.0	8	5	ABB73318 Exemplary

99 23 45.1 8 2 AAY48639 Ray48639 Membrane  
100 23 45.1 8 3 AAY63935 Ray63935 Desmocoll

## ALIGNMENTS

```

RESULT 1
AAB30898
ID AAB30898 standard; peptide; 8 AA.
XX AC AAB30898;
XX DT 02-APR-2001 (first entry)
XX DE Peptide which selectively binds to normal cardiac endothelium.
XX KW Cardiac endothelium; angiogenic factor; vascular endothelium;
XX KW peripheral vascular disease; cardiovascular disease; angiogenesis;
XX KW cardiac neovascularisation.
XX OS Unidentified.
XX PN WO200075329-A1.
XX PD 14-DEC-2000.
XX PF 31-MAY-2000; 2000WO-US014988.
XX PR 07-JUN-1999; 99US-00327045.
XX PA (EDWA-) EDWARDS LIFESCIENCES CORP.
XX PA (BAXT ) BAXTER AG.
XX PI Levine AJ, Mitterer A, Falkner F, Scheifflinger F, Dörner F;
XX DR WPI; 2001-091212/10.
XX PT New chimeric molecules having an angiogenic factor linked to a targeting
XX PT molecule that binds to a vascular endothelium, useful for increasing
XX PT cardiac neovascularization, or treating peripheral vascular and
XX PT cardiovascular diseases.
XX PS Disclosure; Page 27; 67pp; English.
XX CC AAB30895-99 represent targeting molecules, which are used to produce the
XX CC chimeric molecules of the invention. AAB30895-98 selectively bind to
XX CC normal cardiac endothelium. The specification describes a chimeric
XX CC molecule comprising an angiogenic factor linked to a targeting molecule
XX CC that specifically binds to a vascular endothelium. The chimeric molecules
XX CC are useful for treatment of peripheral vascular or cardiovascular
XX CC diseases. Specifically, they are useful for inducing or inhibiting
XX CC angiogenesis, for increasing cardiac neovascularisation in ischemic
XX CC tissue in the peripheral vascular system
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
Db |||||
1 CLHRGNSC 8

RESULT 2
AAB59303
ID AAB59303 standard; peptide; 8 AA.
XX AC AAB59303;
XX DT 21-MAR-2001 (first entry)
XX OS Homo sapiens.

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XX DE Heart homing peptide SEQ ID NO: 9.
XX KW Heart homing peptide; cardiovascular disease; ischaemic disease;
XX KW gene therapy.
XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Disulfide-bond 1..8 /note= "disulfide bond cyclises the peptide"
XX PN WO200075174-A1.
XX PD 14-DEC-2000.
XX PF 31-MAY-2000; 2000WO-US015088.
XX PR 07-JUN-1999; 99US-00326718.
XX PA (BURN-) BURNHAM INST.
XX PI Ruoslahti E, Mackenna DA;
XX DR WPI; 2001-071059/08.
XX PT Novel heart homing peptide that selectively homes to normal ischemic and
XX PT cardiac tissue useful for targeting ischemic tissues for treating
XX PT ischemic and cardiovascular diseases such as atherosclerosis and
XX PT restenosis.
XX PS Claim 2; Page 55; 70pp; English.
XX CC The present invention provides a number of heart homing peptides which
XX CC selectively home to cardiac tissue. These can be used in the treatment of
XX CC cardiovascular and ischemic diseases, such as atherosclerosis,
XX CC thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial
XX CC hypertrophy, congenital heart diseases, ischemic heart disease and
XX CC anginas, acquired valvular/endocardial diseases, primary myocardial
XX CC diseases, cardiac tumours and arrhythmias
XX SQ Sequence 8 AA;

Query Match 100.0%; Score 51; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 1.8e+06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8
Db |||||
1 CLHRGNSC 8

RESULT 3
AAY63252
ID AAY63252 standard; peptide; 8 AA.
XX AC AAY63252;
XX DT 02-MAR-2000 (first entry)
XX DE Protocadherin cell adhesion recognition cyclic peptide SEQ ID NO:2736.
XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;
XX KW inhibition; cadherin extracellular domain; cell adhesion recognition;
XX KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;
XX KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;
XX KW cadherin related neuronal receptor; LI-cadherin; protocadherin;
XX KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;
XX KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;
XX KW neurological disease; cyclic.
XX OS Synthetic.
XX OS Homo sapiens.

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XX FH Key Location/Qualifiers  
 XX FT Disulfide-bond 1. .8  
 XX PN WO9957149-A2.  
 XX PD 11-NOV-1999.  
 XX PF 05-MAY-1999; 99WO-CA000363.  
 XX PR 05-MAY-1998; 98US-00073040.  
 XX PR 06-NOV-1998; 98US-00187859.  
 XX PR 20-JAN-1999; 99US-00234395.  
 XX PR 08-MAR-1999; 99US-00264516.  
 XX PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX PI Blaschuk OW, Gour BJ, Byers S;  
 XX DR WPI; 2000-038791/03.  
 XX PT New cadherin modulating agents, used for modulating nonclassical cadherin  
 PT -mediated functions for treating e.g. cancers, obesity, rheumatoid  
 FT arthritis, multiple sclerosis, diabetes or a neurological disease.  
 XX PS Claim 84; Page 201; 252pp; English.  
 XX CC The present invention describes cadherin modulating agents (MA)  
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
 CC recognition (CAR) sequence. The MAs can be used for modulating  
 CC nonclassical cadherin-mediated functions. They can be used for e.g.  
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
 CC mammal, enhancing delivery of a drug through the skin of a mammal,  
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
 CC expressing cell, preventing or treating obesity in a mammal, stimulating  
 CC blood vessel regression in a mammal, enhancing drug delivery to the  
 CC central nervous system, treating a demyelinating neurological disease,  
 CC increasing vasopermeability in a mammal, enhancing adhesion of  
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing  
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a  
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age  
 CC -related macular degeneration, multiple sclerosis and diabetes. The  
 CC products can also be used for detection and diagnosis and in bioreactors.  
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and  
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in  
 CC the exemplification of the present invention  
 XX PS Sequence 8 AA;  
 XX CC Query Match 60.8%; Score 31; DB 3; Length 8;  
 XX Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 XX Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CLHRGNSC 8  
 Db 1 CINRDNGC 8  
 RESULT 4  
 AAY48836  
 ID AAY48836 standard; peptide; 8 AA.  
 XX AC AAY48836;  
 XX AC AAY48836;  
 XX DT 20-MAR-2003 (revised)  
 XX DT 10-DEC-1999 (first entry)  
 XX DE Membrane dipeptidase-binding retina homing peptide #22.  
 XX

KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;  
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;  
 XX membrane dipeptidase.  
 OS Synthetic.  
 OS Homo sapiens.  
 XX PN WO9946284-A2.  
 XX PD 16-SEP-1999.  
 XX PF 10-MAR-1999; 99WO-US005284.  
 XX PR 13-MAR-1998; 98US-00042107.  
 XX PR 26-FEB-1999; 99US-00258754.  
 XX PA (BURN-) BURNHAM INST.  
 XX PI Rajotte D, Pasqualini R, Ruoslahti EI;  
 XX DR WPI; 1999-571717/48.  
 XX PT New peptides which selectively home to organs or tissues, used for, e.g.  
 FT identifying target ligands and for therapy of pathological conditions.  
 XX PS Claim 28; Page 149; 193pp; English.  
 XX CC The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ or  
 CC tissue, for identifying a target molecule expressed by an organ or tissue  
 CC or for treating an organ or tissue pathology, where the organ or tissue  
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,  
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane  
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are  
 CC used in the exemplification of the present invention. (Updated on 20-MAR-  
 CC 2003 to correct PR field.)  
 XX PS Sequence 8 AA;  
 XX CC Query Match 58.8%; Score 30; DB 2; Length 8;  
 XX Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 XX Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;  
 Qy 1 CLHRGNSC 8  
 Db 1 CMSIGNNC 8  
 RESULT 5  
 AAY61138  
 ID AAY61138 standard; peptide; 8 AA.  
 XX AC AAY61138;  
 XX AC AAY61138;  
 XX DT 02-MAR-2000 (first entry)  
 XX DE Cadherin-6 cell adhesion recognition cyclic peptide SEQ ID NO:1084.  
 XX KW Modulation; nonclassical cadherin mediated cell adhesion; CAR;  
 KW inhibition; cadherin extracellular domain; cell adhesion recognition;  
 KW OB-cadherin; cadherin-5; cadherin-6; cadherin-7; cadherin-8; cadherin-12;  
 KW cadherin-14; cadherin-15; T-cadherin; PB-cadherin;  
 KW cadherin related neuronal receptor; LI-cadherin; protocadherin;  
 KW desmoglein; desmocollin; calcium binding; cancer; tumour; obesity;  
 KW rheumatoid arthritis; multiple sclerosis; diabetes; metastasis;  
 KW neurological disease; cyclic.  
 XX OS Synthetic.  
 XX OS Homo sapiens.  
 XX FH Key Location/Qualifiers  
 XX FT Disulfide-bond 1. .8  
 XX

PN WO9957149-A2.  
 XX  
 PD 11-NOV-1999.  
 XX  
 PF 05-MAY-1999; 99WO-CA000363.  
 XX  
 PR 05-MAY-1998; 98US-00073040.  
 PR 06-NOV-1998; 98US-00187859.  
 PR 20-JAN-1999; 99US-00234395.  
 PR 08-MAR-1999; 99US-00264516.  
 XX  
 PA (ADHE-) ADHEREX TECHNOLOGIES INC.  
 XX  
 PI Blaschuk OW, Gour BJ, Byers S;  
 XX  
 DR WPI; 2000-038791/03.  
 XX  
 PT New cadherin modulating agents, used for modulating nonclassical cadherin  
 PT-mediated functions for treating e.g. cancers, obesity, rheumatoid  
 PT arthritis, multiple sclerosis, diabetes or a neurological disease.  
 XX  
 PS Claim 27; Page 167; 252pp; English.  
 XX  
 CC The present invention describes cadherin modulating agents (MA)  
 CC comprising peptides which comprise a nonclassical cadherin cell adhesion  
 CC recognition (CAR) sequence. The MA can be used for modulating  
 CC nonclassical cadherin-mediated functions. They can be used for e.g.  
 CC inhibiting adhesion of nonclassical-cadherin expressing cells in a  
 CC mammal, enhancing delivery of a drug through the skin of a mammal,  
 CC enhancing delivery of a drug to a tumour in a mammal, treating cancer in  
 CC a mammal, inhibiting metastasis of a cancer in a mammal, inhibiting  
 CC angiogenesis in a mammal, inducing apoptosis in a nonclassical cadherin-  
 CC expressing cell, preventing or treating obesity in a mammal, stimulating  
 CC blood vessel regression in a mammal, enhancing drug delivery to the  
 CC central nervous system, treating a demyelinating neurological disease,  
 CC increasing vasopermeability in a mammal, enhancing adhesion of  
 CC nonclassical cadherin-expressing cells, inhibiting synaptic stability in  
 CC a mammal, or preventing pregnancy in a mammal. They can also be used for  
 CC e.g. enhancing or directing neurite outgrowth, facilitating wound healing  
 CC or reducing scar tissue, or enhancing adhesion of foreign tissue in a  
 CC mammal. They can also be used for treating e.g. psoriasis, arthritis, age  
 CC related macular degeneration, multiple sclerosis and diabetes. The  
 CC products can also be used for detection and diagnosis and in bioreactors.  
 CC AAY60592 to AAY64572 represent specifically claimed peptides, and  
 CC AAY64573 to AAY64643 and AAZ33183 to AAZ33186 represent sequences used in  
 CC the exemplification of the present invention  
 XX  
 SQ Sequence 8 AA;  
 Query Match 58.8%; Score 30; DB 3; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 OY 1 CLHRGNSC 8  
 Db | : || |  
 1 CDSGNC 8  
 RESULT 6  
 ID ABG35010  
 XX ABG35010 standard; peptide; 8 AA.  
 AC ABG35010;  
 XX  
 XX 15-JUL-2002 (first entry)  
 DT Endostatin targeting peptide #9.  
 DE  
 XX Targeting peptide; cancer; Hodgkin's disease; cytostatic;  
 KW immunosuppressive; anti-inflammatory; antiarthritic; antiviral;  
 KW antiatherosclerotic; antidiabetic; antibacterial; diabetes mellitus;  
 KW inflammatory disease; arthritis; atherosclerosis; cancer;  
 KW autoimmune disease; bacterial infection; viral infection.

XX OS Unidentified.  
 XX WO200220722-A2.  
 XX  
 PD 14-MAR-2002.  
 XX  
 PF 07-SEP-2001; 2001WO-US027702.  
 XX  
 PR 08-SEP-2000; 2000US-0231266P.  
 PR 17-JAN-2001; 2001US-00765101.  
 XX  
 PA (TEXA ) UNIV TEXAS SYSTEM.  
 XX  
 PI Arap W, Pasqualini R;  
 XX  
 DR WPI; 2002-383050/41.  
 XX  
 PT Identifying targeting peptides useful for treating e.g. diabetes  
 PT mellitus, inflammatory diseases, cancer, or autoimmune diseases,  
 PT comprises exposing a sample to a phage display library and recovering  
 PT phage bound to the sample.  
 XX  
 PS Claim 56; Page 238; 298pp; English.  
 XX  
 CC This invention relates to a novel method for identifying disease  
 CC targeting peptides. The method comprises exposing a sample from an organ,  
 CC tissue or cell type of interest, to a phage display library and  
 CC recovering phage bound to the sample (the phage expresses targeting  
 CC peptides). The peptides identified by the method of the invention may  
 CC have cytostatic, immunosuppressive, anti-inflammatory, antiarthritic,  
 CC antiatherosclerotic, antidiabetic, antibacterial and antiviral  
 CC activities. The methods and composition are useful for identifying  
 CC targeting peptides and one or more receptors for a targeting peptide. The  
 CC targeting peptides are used for selective delivery of therapeutic agents,  
 CC including gene therapy vectors and fusion proteins, to specific organs,  
 CC tissues, or cell types in subject. The targeting peptide may also be used  
 CC for treating diseases such as diabetes mellitus, inflammatory diseases,  
 CC arthritis, atherosclerosis, cancer, autoimmune diseases, bacterial and  
 CC viral infections and Hodgkin's disease. The present sequence represents a  
 CC targeting peptide of the invention  
 XX  
 SQ Sequence 8 AA;  
 Query Match 58.8%; Score 30; DB 5; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;  
 OY 1 CLHRGNSC 8  
 Db | : || |  
 1 CMNRGSTC 8  
 RESULT 7  
 ABJ04479  
 ID ABJ04479 standard; peptide; 8 AA.  
 XX  
 AC ABJ04479;  
 XX  
 XX 24-OCT-2002 (first entry)  
 DT HUVEC cell targeting peptide 26.  
 DE  
 XX BRASIL; targeting peptide; bacterial infection;  
 KW Biopanning and Rapid Analysis of Selective Interactant Ligands; diabetes;  
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;  
 KW viral infection; cardiovascular disease; degenerative disease.  
 XX Unidentified.  
 OS  
 XX WO200220822-A2.  
 PN  
 XX 14-MAR-2002.  
 PD

```

XX PF 07-SEP-2001; 2001WO-US028124.
XX XX
XX PR 08-SEP-2000; 2000US-0231266P.
XX PR 17-JAN-2000; 2001US-00765101.
XX XX
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX XX
XX PI Arap W, Pasqualini R;
XX XX
XX DR WPI; 2002-404697/43.
XX XX
XX PT Identification of targeting peptides that can be used to treat diseases
XX PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis
XX PT of Selective Ligands) method comprises a single differential
XX PT centrifugation step.
XX XX
XX PS Example 2; Page 64; 167pp; English.
XX XX
XX CC The invention comprises a method (BRASIL - Biopanning and Rapid Analysis
XX CC of Selective Interactive Ligands) to obtain a targeting peptide. The
XX CC BRASIL method of the invention involves: exposing a target to a phage
XX CC display library in a first phase; exposing the first phase to a second
XX CC phase; and separating the phage bound to the target from unbound phage.
XX CC The BRASIL method of the invention allows cell phages to be separated
XX CC from the remaining unbound phage in a single differential centrifugation
XX CC step. When compared to conventional cell panning methods, the BRASIL
XX CC method shows a significant increase in recovery of specific phage and a
XX CC substantial decrease in background. The BRASIL method is useful for
XX CC identifying targeting peptides. The targeting peptides identified by the
XX CC method of the invention are useful for treating disease states, such as:
XX CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune
XX CC disease; bacterial infection; viral infection; cardiovascular disease and
XX CC degenerative disease. The present amino acid sequence represents a
XX CC targeting peptide of the invention
XX SQ Sequence 8 AA;

    Query Match      58.8%; Score 30; DB 5; Length 8;
    Best Local Similarity 50.0%; Pred. No. 1.8e+06;
    Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
   |::|||
Db 1 CSYKANSC 8

RESULT 8
AAAY48662
ID AAY48662 standard; peptide; 8 AA.
XX XX
XX AC AAY48662;
XX XX
XX DT 20-MAR-2003 (revised)
XX DT 10-DEC-1999 (first entry)
XX XX
XX DE Membrane dipeptidase-binding lung homing peptide #33.
XX XX
XX KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
XX KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
XX KW membrane dipeptidase.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9946284-A2.
XX XX
XX PD 16-SEP-1999.
XX XX
XX PF 10-MAR-1999; 99WO-US005284.
XX XX
XX PR 13-MAR-1998; 98US-00042107.
XX PR 26-FEB-1999; 99US-00258754.
XX XX
XX PA (BURN-) BURNHAM INST.
XX XX
XX PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX XX
XX DR WPI; 1999-571717/48.
XX XX
XX PT New peptides which selectively home to organs or tissues, used for, e.g.
XX PT identifying target ligands and for therapy of pathological conditions.
XX XX
XX PS Claim 27; Page 150; 193pp; English.
XX XX
XX CC The present invention describes peptides that selectively home to a
XX CC tissue or organ. The peptides can be used for identifying an organ or

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XX PA (BURN-) BURNHAM INST.
XX XX
XX PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX XX
XX DR WPI; 1999-571717/48.
XX XX
XX PT New peptides which selectively home to organs or tissues, used for, e.g.
XX PT identifying target ligands and for therapy of pathological conditions.
XX XX
XX PS Example 6; Page 144; 193pp; English.
XX XX
XX CC The present invention describes peptides that selectively home to a
XX CC tissue or organ. The peptides can be used for identifying an organ or
XX CC tissue, for identifying a target molecule expressed by an organ or tissue
XX CC or for treating an organ or tissue pathology, where the organ or tissue
XX CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,
XX CC adrenal gland, liver, and lymph node. The peptide bind to the membrane
XX CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are
XX CC used in the exemplification of the present invention. (Updated on 20-MAR-
XX CC 2003 to correct PR field.)
XX SQ Sequence 8 AA;

    Query Match      56.9%; Score 29; DB 2; Length 8;
    Best Local Similarity 50.0%; Pred. No. 1.8e+06;
    Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
   |::|||
Db 1 CRHESSC 8

RESULT 9
AAAY48879
ID AAY48879 standard; peptide; 8 AA.
XX XX
XX AC AAY48879;
XX XX
XX DT 20-MAR-2003 (revised)
XX DT 10-DEC-1999 (first entry)
XX XX
XX DE Membrane dipeptidase-binding retina homing peptide #65.
XX XX
XX KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;
XX KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;
XX KW membrane dipeptidase.
XX XX
XX OS Synthetic.
XX OS Homo sapiens.
XX XX
XX PN WO9946284-A2.
XX XX
XX PD 16-SEP-1999.
XX XX
XX PF 10-MAR-1999; 99WO-US005284.
XX XX
XX PR 13-MAR-1998; 98US-00042107.
XX PR 26-FEB-1999; 99US-00258754.
XX XX
XX PA (BURN-) BURNHAM INST.
XX XX
XX PI Rajotte D, Pasqualini R, Ruoslahti EI;
XX XX
XX DR WPI; 1999-571717/48.
XX XX
XX PT New peptides which selectively home to organs or tissues, used for, e.g.
XX PT identifying target ligands and for therapy of pathological conditions.
XX XX
XX PS Claim 27; Page 150; 193pp; English.
XX XX
XX CC The present invention describes peptides that selectively home to a
XX CC tissue or organ. The peptides can be used for identifying an organ or

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CC tissue, for identifying a target molecule expressed by an organ or tissue  
CC or for treating an organ or tissue pathology, where the organ or tissue  
CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,  
CC adrenal gland, liver, and lymph node. The peptide bind to the membrane  
CC dipeptidase (MDP). AA48618 to AA49066 represent sequences which are  
CC used in the exemplification of the present invention. (Updated on 20-MAR-  
CC 2003 to correct PR field.)  
XX  
SQ

Sequence 8 AA;

Query Match 54.9%; Score 28; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
| : : : |  
DB 1 CRYKGPSC 8

## RESULT 10

ABB98083  
ID ABB98083 standard; peptide; 8 AA.

XX AC ABB98083;  
XX  
DT 02-OCT-2002 (first entry)  
XX  
DE Fc effector peptide #9.

XX Fc effector; antibody; immunoglobulin; Fc region; binding; vaccine.

XX Unidentified.

XX WO200244215-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-GB005301.

XX 01-DEC-2000; 2000GB-00029407.

XX (COCK/) COCKBAIN J.  
XX (BREK/) BREKKE O H A.  
XX (LAUV/) LAUVRAK V.  
XX (SAND/) SANDLIE I.

XX Brekke OHA, Lauvrak V, Sandlie I;

XX WPI; 2002-527704/56.

XX Binding molecules useful in therapy, diagnosis and imaging, have  
PT polypeptides forming binding sites for target molecules, and Fc effector  
PT peptides displaying functions associated with constant regions of  
PT immunoglobulin heavy chains.

XX Claim 10; Page 16; 77pp; English.

XX The invention relates to a binding molecule comprising one or more  
CC polypeptides which form a binding site capable of binding a target  
CC molecule, and an Fc effector peptide displaying one or more effector  
CC functions associated with the constant region (Fc) of an immunoglobulin  
CC heavy chain. Peptides of the invention are useful in therapy, diagnosis  
CC or imaging. Therapy using peptides of the invention is likely to be more  
CC effective and less immunogenic than, for example, the targeting of other  
CC therapeutic fusion proteins, as they induce a response based on that  
CC which would be induced by natural intact immunoglobulins in the body. The  
CC Fc effector peptides binds to FcRn receptors that mediate retention of  
CC antibodies in intracellular vesicles in endothelial cells lining blood  
CC vessels in vivo, therefore the binding molecules comprising FcRn-binding  
CC peptides will remain in the body circulation longer than normal antibody  
CC fragments. Peptides of the invention may also be utilised in vaccines.  
CC The current sequence represents a preferred Fc effector peptide of the  
CC invention, which has the ability to bind Fc receptors

XX SQ Sequence 8 AA;

Query Match 54.9%; Score 28; DB 5; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
| : : : |  
DB 1 CLRSGSGC 8

## RESULT 11

ABB98084  
ID ABB98084 standard; peptide; 8 AA.

XX AC ABB98084;

XX 02-OCT-2002 (first entry)

XX Fc effector peptide #10.

XX Fc effector; antibody; immunoglobulin; Fc region; binding; vaccine.

XX Unidentified.

XX WO200244215-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-GB005301.

XX 01-DEC-2000; 2000GB-00029407.

XX (COCK/) COCKBAIN J.  
XX (BREK/) BREKKE O H A.  
XX (LAUV/) LAUVRAK V.  
XX (SAND/) SANDLIE I.

XX Brekke OHA, Lauvrak V, Sandlie I;

XX WPI; 2002-527704/56.

XX Binding molecules useful in therapy, diagnosis and imaging, have  
PT polypeptides forming binding sites for target molecules, and Fc effector  
PT peptides displaying functions associated with constant regions of  
PT immunoglobulin heavy chains.

XX Claim 10; Page 16; 77pp; English.

XX The invention relates to a binding molecule comprising one or more  
CC polypeptides which form a binding site capable of binding a target  
CC molecule, and an Fc effector peptide displaying one or more effector  
CC functions associated with the constant region (Fc) of an immunoglobulin  
CC heavy chain. Peptides of the invention are useful in therapy, diagnosis  
CC or imaging. Therapy using peptides of the invention is likely to be more  
CC effective and less immunogenic than, for example, the targeting of other  
CC therapeutic fusion proteins, as they induce a response based on that  
CC which would be induced by natural intact immunoglobulins in the body. The  
CC Fc effector peptides binds to FcRn receptors that mediate retention of  
CC antibodies in intracellular vesicles in endothelial cells lining blood  
CC vessels in vivo, therefore the binding molecules comprising FcRn-binding  
CC peptides will remain in the body circulation longer than normal antibody  
CC fragments. Peptides of the invention may also be utilised in vaccines.  
CC The current sequence represents a preferred Fc effector peptide of the  
CC invention, which has the ability to bind Fc receptors

XX SQ Sequence 8 AA;

Query Match 54.9%; Score 28; DB 5; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;



QY 1 CLHRGNSC 8  
 || | : |  
 Db 1 CLRSGRAC 8

## RESULT 12

ABJ04391  
 ID ABJ04391 standard; peptide; 8 AA.

XX AC ABJ04391;

DT 24-OCT-2002 (first entry)

XX HUVEC cell targeting peptide 3.

XX BRASIL; targeting peptide; bacterial infection;

KW Biopanning and Rapid Analysis of Selective Interactive Ligands; diabetes;  
 KW inflammatory arthritis; atherosclerosis; cancer; autoimmune disease;  
 KW viral infection; cardiovascular disease; degenerative disease.

OS Unidentified.

PN WO200220822-A2.

XX 14-MAR-2002.

XX 07-SEP-2001; 2001WO-US028124.

XX 08-SEP-2000; 2000US-0231266P.

PR 17-JAN-2001; 2001US-00765101.

XX (TEXA ) UNIV TEXAS SYSTEM.

XX Arap W, Pasqualini R;

XX WPI; 2002-404697/43.

XX Identification of targeting peptides that can be used to treat diseases  
 PT e.g. cancer and arthritis, by the BRASIL (Biopanning and Rapid Analysis  
 PT of Selective Ligands) method comprises a single differential  
 PT centrifugation step.

XX Claim 78; Page 100; 167pp; English.

XX The invention comprises a method (BRASIL - Biopanning and Rapid Analysis  
 CC of Selective Interactive Ligands) to obtain a targeting peptide. The  
 CC BRASIL method of the invention involves: exposing a target to a phage  
 CC display library in a first phase; exposing the first phase to a second  
 CC phase; and separating the phage bound to the target from unbound phage.  
 CC The BRASIL method of the invention allows cell phages to be separated  
 CC from the remaining unbound phage in a single differential centrifugation  
 CC step. When compared to conventional cell panning methods, the BRASIL  
 CC method shows a significant increase in recovery of specific phage and a  
 CC substantial decrease in background. The BRASIL method is useful for  
 CC identifying targeting peptides. The targeting peptides identified by the  
 CC method of the invention are useful for treating disease states, such as:  
 CC diabetes; inflammatory arthritis; atherosclerosis; cancer; autoimmune  
 CC disease; bacterial infection; viral infection; cardiovascular disease and  
 CC degenerative disease. The present amino acid sequence represents a  
 CC targeting peptide of the invention

XX Sequence 8 AA;

Query Match 52.9%; Score 27; DB 5; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
 || | : |  
 Db 1 CLGKGSVC 8

## RESULT 13

ABB98080  
 ID ABB98080 standard; peptide; 8 AA.

XX ABB98080;

XX 02-OCT-2002 (first entry)

XX Fc effector peptide #6.

XX Fc effector; antibody; immunoglobulin; Fc region; binding; vaccine.

XX Unidentified.

XX WO200244215-A2.

XX 06-JUN-2002.

XX 30-NOV-2001; 2001WO-GB005301.

XX 01-DEC-2000; 2000GB-00029407.

XX (COCK/) COCKBAIN J.

XX (BREK/) BREKKE O H A.

XX (LAUV/) LAUVRAK V.

XX (SAND/) SANDLIE I.

XX Brekke OHA, Lauvrak V, Sandlie I;

XX WPI; 2002-527704/56.

XX Binding molecules useful in therapy, diagnosis and imaging, have  
 PT polypeptides forming binding sites for target molecules, and Fc effector  
 PT peptides displaying functions associated with constant regions of  
 PT immunoglobulin heavy chains.

XX Claim 10; Page 16; 77pp; English.

XX The invention relates to a binding molecule comprising one or more  
 CC polypeptides which form a binding site capable of binding a target  
 CC molecule, and an Fc effector peptide displaying one or more effector  
 CC functions associated with the constant region (Fc) of an immunoglobulin  
 CC heavy chain. Peptides of the invention are useful in therapy, diagnosis  
 CC or imaging. Therapy using peptides of the invention is likely to be more  
 CC effective and less immunogenic than, for example, the targeting of other  
 CC therapeutic fusion proteins, as they induce a response based on that  
 CC which would be induced by natural intact immunoglobulins in the body. The  
 CC Fc effector peptides binds to FcRn receptors that mediate retention of  
 CC antibodies in intracellular vesicles in endothelial cells lining blood  
 CC vessels in vivo, therefore the binding molecules comprising FcRn-binding  
 CC peptides will remain in the body circulation longer than normal antibody  
 CC fragments. Peptides of the invention may also be utilised in vaccines.  
 CC The current sequence represents a preferred Fc effector peptide of the  
 CC invention, which has the ability to bind Fc receptors

XX Sequence 8 AA;

Query Match 52.9%; Score 27; DB 5; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
 || | : |  
 Db 1 CLRSGRGC 8

## RESULT 14

AAW54868  
 ID AAW54868 standard; protein; 7 AA.

XX AAW54868;

XX 11-SEP-1998 (first entry)

DE Homo sapiens Fyb71 peptide.  
 XX GP-FY protein; Fyb71-81; duffy blood group; antigen; alpha; beta;  
 KW alternative splicing; RBC; red blood cell; malaria; treatment.  
 XX  
 XX Homo sapiens.  
 XX OS  
 PN WO9821224-A1.  
 XX PD  
 XX 22-MAY-1998.  
 XX PF  
 XX 14-NOV-1997; 97WO-US021067.  
 XX PR  
 XX 15-NOV-1996; 96US-00749543.  
 XX (NYBL-) NEW YORK BLOOD CENT INC.  
 XX PA  
 XX Pogo OA, Chaudhuri A;  
 XX PI  
 XX WPI; 1998-297854/26.  
 XX DR  
 XX Nucleic acid encoding gp-Fy, Duffy antigen proteins - used to prevent  
 PT vivax malaria and to regulate erythrocyte, neural or renal function.  
 XX PF  
 XX Example 10; Page 27; 87pp; English.  
 XX PS  
 XX The sequence is that of a peptide encoded by Fyb71 which was used in the  
 CC isolation of gp-Fy mRNA  
 XX CC  
 XX Sequence 7 AA;  
 SQ  
 Query Match 51.0%; Score 26; DB 2; Length 7;  
 Best Local Similarity 100.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 CLHR 4  
 ||||  
 Db 4 CLHR 7  
 RESULT 15  
 AAR96348  
 ID AAR96348 standard; peptide; 8 AA.  
 XX  
 AC AAR96348;  
 XX  
 DT 05-JUL-1996 (first entry)  
 XX  
 DE RGD cyclic peptide, binds alpha-v,beta3 integrin receptor.  
 XX  
 KW RGD-containing peptide; alpha-v, beta-3 integrin receptor; osteoclast;  
 KW matrix; bone; inhibition; bone resorption; promote; endothelial cell;  
 KW smooth muscle cell; restenosis; angiogenesis; cyclic.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1. 8  
 FT Modified-site 1  
 FT /note= "Acyl-Cys"  
 FT Modified-site 7  
 FT /label= OTHER  
 FT /note= "OTHER = 1,2,3,4-Tetrahydroisoquinoline-3-  
 FT carboxylic acid"  
 FT Modified-site 8  
 FT /note= "Amidated C-terminal"  
 XX  
 PN WO9528426-A2.  
 XX  
 XX 26-OCT-1995.  
 PD  
 XX  
 XX 12-APR-1995; 95WO-US004741.  
 PF  
 XX

PR 13-APR-1994; 94US-00227316.  
 PR 08-SEP-1994; 94US-00303052.  
 XX  
 PA (LJOL-) LA JOLLA CANCER RES FOUND.  
 XX  
 XX Cheng S, Ingram R, Mullen D, Tschopp J;  
 XX PI  
 XX WPI; 1995-373767/48.  
 XX DR  
 XX  
 XX Altering alpha-v, beta-3 integrin receptor-mediated binding of cell to  
 PT matrix - using conformationally restrained peptide of RGD type, e.g. for  
 PT treating inappropriate angiogenesis or for inhibiting bone resorption.  
 XX  
 XX Claim 84; Page 78; 99pp; English.  
 PS  
 XX The sequences given in AAR96301-417 are non-naturally occurring RGD-  
 CC containing peptides which alter the alpha-v, beta-3 integrin receptor  
 CC binding of a cell to a matrix, such as the binding of an osteoclast to a  
 CC matrix such as bone. These peptides inhibit bone resorption and can  
 CC inhibit or promote alpha-v, beta-3-mediated cell attachment depending on  
 CC whether they are present in the cell in a soluble form or are bound to a  
 CC solid substrate. These peptides can be used in the amelioration of the  
 CC severity of a pathology involving alpha-v, beta-3 receptor-mediated  
 CC binding of a cell, such as an osteoclast, endothelial cell or smooth  
 CC muscle cell to a matrix. They are used for treating conditions associated  
 CC with restenosis or inappropriate or insufficient angiogenesis, or for  
 CC inhibiting osteoclast binding to the matrix  
 XX  
 XX Sequence 8 AA;  
 SQ  
 Query Match 51.0%; Score 26; DB 2; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.8e+06;  
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 CLHRGNSC 8  
 ||||  
 Db 1 CAARGTXC 8  
 Search completed: August 3, 2005, 12:16:47  
 Job time : 163 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:09:38 ; Search time 41 Seconds  
(without alignments)  
14.566 Million cell updates/sec

Title: US-09-910-582B-9  
Perfect score: 51  
Sequence: 1 CLHRGNSC 8

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 77247

Minimum DB seq length: 0  
Maximum DB seq length: 8

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

- Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTCUS COMB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	31	60.8	8	4	US-09-839-542B-2736
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5	30	58.8	8	3	US-09-042-107-240
6	30	58.8	8	3	US-09-187-859-1084
7	30	58.8	8	4	US-09-839-542B-1084
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9	30	58.8	8	4	US-09-676-475A-240
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11	29	56.9	8	3	US-09-042-107-33
12	29	56.9	8	4	US-09-722-250D-33
13	29	56.9	8	4	US-09-676-475A-33
14	28	54.9	8	3	US-09-258-754-257
15	28	54.9	8	3	US-09-042-107-257
16	28	54.9	8	4	US-09-722-250D-257
17	28	54.9	8	4	US-09-676-475A-257
18	26	51.0	7	2	US-08-749-526-12
19	26	51.0	8	1	US-08-526-710-4
20	26	51.0	8	2	US-08-421-695A-125
21	26	51.0	8	3	US-08-862-855-4
22	26	51.0	8	3	US-09-226-985-4
23	26	51.0	8	3	US-09-227-906-4
24	26	51.0	8	3	US-09-187-859-3086
25	26	51.0	8	4	US-09-839-542B-3086
26	26	51.0	8	4	US-09-535-852-430
27	26	51.0	8	4	US-09-428-082B-1091

## ALIGNMENTS

RESULT 1  
 US-09-326-718-9  
 ; Sequence 9, Application US/09326718  
 ; Patent No. 6303573  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruoslahti, Erkki  
 ; APPLICANT: MacKenna, Deidre A.  
 ; TITLE OF INVENTION: Heart Homing Peptides and Methods of  
 ; TITLE OF INVENTION: Using Same  
 ; FILE REFERENCE: P-LJ 3512  
 ; CURRENT APPLICATION NUMBER: US/09/326,718  
 ; CURRENT FILING DATE: 1999-06-07  
 ; NUMBER OF SEQ ID NOS: 15  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 9  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: synthetic construct  
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 US-09-326-718-9

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QY 1 CLHRGNSC 8  
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 Db 1 CLHRGNSC 8

RESULT 2  
 US-09-187-859-2736  
 ; Sequence 2736, Application US/09187859A  
 ; Patent No. 6358920  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Blaschuk, Orest W.  
 ; APPLICANT: Gour, Barbara J.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
 ; FILE REFERENCE: 100086.407C1  
 ; CURRENT APPLICATION NUMBER: US/09/187,859A  
 ; CURRENT FILING DATE: 1998-11-06  
 ; NUMBER OF SEQ ID NOS: 4052  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2736  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Representative cyclic modulating agent based on  
 ; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence  
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 US-09-187-859-2736

Query Match 60.8%; Score 31; DB 3; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
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 Db 1 CINRDNGC 8

RESULT 3  
 US-09-839-542B-2736  
 ; Sequence 2736, Application US/09839542B  
 ; Patent No. 6569996  
 ; GENERAL INFORMATION:

; APPLICANT: Blaschuk, Orest W.  
 ; APPLICANT: Symonds, James Matthew  
 ; APPLICANT: Gour, Barbara J.  
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
 ; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
 ; FILE REFERENCE: 100086.407D1  
 ; CURRENT APPLICATION NUMBER: US/09/839,542B  
 ; CURRENT FILING DATE: 2001-04-20  
 ; NUMBER OF SEQ ID NOS: 4052  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 2736  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Representative cyclic modulating agent based on  
 ; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence  
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 US-09-839-542B-2736

Query Match 60.8%; Score 31; DB 4; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
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 Db 1 CINRDNGC 8

RESULT 4  
 US-09-258-754-240  
 ; Sequence 240, Application US/09258754  
 ; Patent No. 6174687  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruoslahti, Erkki  
 ; APPLICANT: Pasqualini, Renata  
 ; APPLICANT: Rajotte, Daniel  
 ; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
 ; TITLE OF INVENTION: Membrane Dipeptidase  
 ; FILE REFERENCE: P-LJ 3443  
 ; CURRENT APPLICATION NUMBER: US/09/258,754  
 ; CURRENT FILING DATE: 1999-02-26  
 ; EARLIER APPLICATION NUMBER: 09/042,107  
 ; EARLIER FILING DATE: 1998-03-13  
 ; NUMBER OF SEQ ID NOS: 452  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 240  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
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 US-09-258-754-240

Query Match 58.8%; Score 30; DB 3; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
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 Db 1 CMSLGNNC 8

RESULT 5  
 US-09-042-107-240  
 ; Sequence 240, Application US/09042107  
 ; Patent No. 6232287  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruoslahti, Erkki  
 ; APPLICANT: Pasqualini, Renata  
 ; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
 ; TITLE OF INVENTION: Tissues  
 ; FILE REFERENCE: P-LJ 2892  
 ; CURRENT APPLICATION NUMBER: US/09/042,107

; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 240  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-240

Query Match 58.8%; Score 30; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
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Db 1 CMSLGNCC 8

RESULT 6  
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; Sequence 1084, Application US/09187859A  
; Patent No. 6358920  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C1  
; CURRENT APPLICATION NUMBER: US/09/187.859A  
; CURRENT FILING DATE: 1998-11-06  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1084  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-187-859-1084

Query Match 58.8%; Score 30; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
|: |||  
Db 1 CIDSNGCC 8

RESULT 7  
US-09-839-542B-1084  
; Sequence 1084, Application US/09839542B  
; Patent No. 6569996  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407D1  
; CURRENT APPLICATION NUMBER: US/09/839.542B  
; CURRENT FILING DATE: 2001-04-20  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1084  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on

; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-09-839-542B-1084

Query Match 58.8%; Score 30; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
|: |||  
Db 1 CIDSNGCC 8

RESULT 8  
US-09-722-250D-240  
; Sequence 240, Application US/09722250D  
; Patent No. 6610651  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 4514  
; CURRENT APPLICATION NUMBER: US/09/722.250D  
; CURRENT FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: US 09/042,107  
; NUMBER OF SEQ ID NOS: 437  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 240  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-722-250D-240

Query Match 58.8%; Score 30; DB 4; Length 8;  
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Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
|: |||  
Db 1 CMSLGNCC 8

RESULT 9  
US-09-676-475A-240  
; Sequence 240, Application US/09676475A  
; Patent No. 6784153  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Dipeptidase  
; FILE REFERENCE: P-LA 4377  
; CURRENT APPLICATION NUMBER: US/09/676.475A  
; CURRENT FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 09/042,107  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 240  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-676-475A-240

Query Match 58.8%; Score 30; DB 4; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Qy 1 CLHRGNSC 8
Db 1 CMSGNMC 8

RESULT 10
US-09-258-754-33
; Sequence 33, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
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; SEQ ID NO 33
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-33

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Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
Db 1 CRHESSC 8

RESULT 13
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; Sequence 33, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 33
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-33

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Best Local Similarity 50.0%; Pred. No. 4.1e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8
Db 1 CRHESSC 8

RESULT 14
US-09-258-754-257
; Sequence 257, Application US/09258754
; Patent No. 6174687
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
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; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Dipeptidase  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 257  
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; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-257

Query Match 54.9%; Score 28; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
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Db 1 CRYKGPSC 8

RESULT 15  
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; Sequence 257, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 257  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-257

Query Match 54.9%; Score 28; DB 3; Length 8;  
Best Local Similarity 50.0%; Pred. No. 4.1e+05;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

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Db 1 CRYKGPSC 8

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

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Title: US-09-910-582B-9  
Perfect score: 51  
Sequence: 1 CLHRGNSC 8

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Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

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Listing first 100 summaries

Database : Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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5	31	60.8	8	15	US-10-395-032-2736
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12	29	56.9	8	17	US-10-838-289-136	Sequence 136, App
13	29	56.9	8	17	US-10-607-595-33	Sequence 33, Appl
14	28	54.9	8	16	US-10-433-452A-9	Sequence 9, Appl
15	28	54.9	8	16	US-10-433-452A-10	Sequence 10, Appl
16	28	54.9	8	17	US-10-838-289-314	Sequence 314, App
17	28	54.9	8	17	US-10-607-595-257	Sequence 257, App
18	28	54.9	8	17	US-10-923-940-10	Sequence 10, Appl
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23	27	52.9	8	17	US-10-923-940-9	Sequence 9, Appl
24	27	52.9	8	17	US-10-923-940-11	Sequence 11, Appl
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27	26	51.0	8	15	US-10-395-032-3086	Sequence 3086, Ap
28	26	51.0	8	15	US-10-464-302-52	Sequence 52, Appl
29	26	51.0	8	15	US-10-609-217-1091	Sequence 1091, Ap
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34	26	51.0	8	15	US-10-645-761-1091	Sequence 1091, Ap
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38	26	51.0	8	16	US-10-433-452A-11	Sequence 11, Appl
39	26	51.0	8	16	US-10-433-452A-56	Sequence 56, Appl
40	26	51.0	8	16	US-10-654-578-430	Sequence 430, App
41	26	51.0	8	17	US-10-943-372-4	Sequence 4, Appl
42	26	51.0	8	17	US-10-838-289-2	Sequence 2, Appl
43	26	51.0	8	18	US-10-645-784-1091	Sequence 1091, Ap
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47	25	49.0	8	13	US-10-006-982-18	Sequence 18, Appl
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49	25	49.0	8	14	US-10-006-869-3653	Sequence 3653, Ap
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51	25	49.0	8	15	US-10-359-546-28	Sequence 28, Appl
52	25	49.0	8	15	US-10-395-032-3553	Sequence 3553, Ap
53	25	49.0	8	15	US-10-425-557-42	Sequence 42, Appl
54	25	49.0	8	15	US-10-363-208-98	Sequence 98, Appl
55	25	49.0	8	15	US-10-412-701-42	Sequence 42, Appl
56	25	49.0	8	16	US-10-433-452A-8	Sequence 8, Appl
57	25	49.0	8	16	US-10-632-678-42	Sequence 42, Appl
58	25	49.0	8	16	US-10-654-578-938	Sequence 938, App
59	25	49.0	8	16	US-10-759-507-307	Sequence 307, App
60	25	49.0	8	16	US-10-759-507-307	Sequence 307, App
61	24	47.1	8	9	US-09-769-145-43	Sequence 43, Appl
62	24	47.1	8	11	US-09-922-227-25	Sequence 25, Appl
63	24	47.1	8	11	US-09-922-227-26	Sequence 26, Appl
64	24	47.1	8	13	US-10-006-982-19	Sequence 19, Appl
65	24	47.1	8	14	US-10-105-008-43	Sequence 43, Appl
66	24	47.1	8	14	US-10-006-869-3101	Sequence 3101, Ap
67	24	47.1	8	14	US-10-006-869-3359	Sequence 3359, Ap
68	24	47.1	8	15	US-10-359-546-51	Sequence 51, Appl
69	24	47.1	8	15	US-10-395-032-3101	Sequence 3101, Ap
70	24	47.1	8	15	US-10-395-032-3359	Sequence 3359, Ap
71	24	47.1	8	15	US-10-425-557-43	Sequence 43, Appl
72	24	47.1	8	15	US-10-363-208-81	Sequence 81, Appl
73	24	47.1	8	15	US-10-412-701-43	Sequence 43, Appl
74	24	47.1	8	16	US-10-433-452A-7	Sequence 7, Appl
75	24	47.1	8	16	US-10-632-678-43	Sequence 43, Appl
76	24	47.1	8	16	US-10-654-578-445	Sequence 445, App
77	24	47.1	8	16	US-10-654-578-703	Sequence 703, App
78	24	47.1	8	17	US-10-943-372-25	Sequence 25, Appl
79	24	47.1	8	17	US-10-943-372-26	Sequence 26, Appl
80	24	47.1	8	17	US-10-838-289-23	Sequence 23, Appl
81	24	47.1	8	17	US-10-838-289-24	Sequence 24, Appl
82	24	47.1	8	17	US-10-838-289-315	Sequence 315, App
83	24	47.1	8	17	US-10-607-595-258	Sequence 258, App
84	23	45.1	6	16	US-10-865-661-1	Sequence 1, Appl

85 23 45.1 7 18 US-10-755-415-355 Sequence 355, App  
86 23 45.1 8 11 US-09-896-784-31 Sequence 31, Appl  
87 23 45.1 8 14 US-10-215-168-9 Sequence 9, Appl  
88 23 45.1 8 14 US-10-006-869-3347 Sequence 3347, Ap  
89 23 45.1 8 15 US-10-395-032-3347 Sequence 3347, Ap  
90 23 45.1 8 16 US-10-433-452A-12 Sequence 12, Appl  
91 23 45.1 8 16 US-10-363-204-241 Sequence 241, App  
92 23 45.1 8 16 US-10-654-578-691 Sequence 691, App  
93 23 45.1 8 17 US-10-838-289-145 Sequence 145, App  
94 23 45.1 8 17 US-10-607-595-40 Sequence 40, Appl  
95 23 45.1 8 17 US-10-488-779A-44 Sequence 44, Appl  
96 22.5 44.1 7 14 US-10-006-869-3085 Sequence 3085, Ap  
97 22.5 44.1 7 15 US-10-395-032-3085 Sequence 3085, Ap  
98 22.5 44.1 7 16 US-10-654-578-429 Sequence 429, App  
99 22 43.1 6 9 US-09-821-831-41 Sequence 41, Appl  
100 22 43.1 6 17 US-10-921-065-41 Sequence 41, Appl

## ALIGNMENTS

RESULT 1  
US-09-782-650-4  
; Sequence 4, Application US/09782650  
; Patent No. US2002001950A1  
; GENERAL INFORMATION:  
; APPLICANT: Levine, Arnold J.  
; APPLICANT: Mitterer, Artur  
; APPLICANT: Falkner, Falko-Guenter  
; APPLICANT: Scheiflinger, Friedrich  
; APPLICANT: Dörner, Friedrich  
; APPLICANT: Edwards Lifesciences Corporation  
; TITLE OF INVENTION: Targeted Angiogenesis  
; FILE REFERENCE: 20553D-000611US  
; CURRENT APPLICATION NUMBER: US/09/782,650  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: US 09/324,079  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: US 09/327,045  
; PRIOR FILING DATE: 1999-06-07  
; PRIOR APPLICATION NUMBER: PCT/US00/14988  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:targeting  
; OTHER INFORMATION: molecule  
US-09-782-650-4

Query Match 100.0%; Score 51; DB 9; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
| | | | | | | |  
Db 1 CLHRGNSC 8

RESULT 2  
US-09-910-582b-9  
; Sequence 9, Application US/09910582B  
; Publication No. US20030045476A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Mackenna, Deirdre A.  
; TITLE OF INVENTION: Heart Homing Conjugates  
; FILE REFERENCE: P-LJ 4857  
; CURRENT APPLICATION NUMBER: US/09/910,582B  
; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/326,718  
; PRIOR FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-910-582B-9

Query Match 100.0%; Score 51; DB 10; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
| | | | | | | |  
Db 1 CLHRGNSC 8

RESULT 3  
US-10-838-289-37  
; Sequence 37, Application US/10838289  
; Publication No. US20050058603A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Jimming  
; APPLICANT: Ai, Hua  
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
; TITLE OF INVENTION: NANOSHELLS  
; FILE REFERENCE: CMRU-P01-040  
; CURRENT APPLICATION NUMBER: US/10/838,289  
; CURRENT FILING DATE: 2004-05-03  
; PRIOR APPLICATION NUMBER: US 60/502,429  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: US 60/467,389  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 756  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 37  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Heart homing peptide  
US-10-838-289-37

Query Match 100.0%; Score 51; DB 17; Length 8;  
Best Local Similarity 100.0%; Pred. No. 1.6e+06;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
| | | | | | | |  
Db 1 CLHRGNSC 8

RESULT 4  
US-10-006-869-2736  
; Sequence 2736, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2736  
; LENGTH: 8

; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence  
US-10-006-869-2736

Query Match 60.8%; Score 31; DB 14; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8  
|:|:|  
Db 1 C1NRDNGC 8

RESULT 5  
US-10-395-032-2736  
; Sequence 2736, Application US/10395032  
; Publication No. US20030229199A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C9  
; CURRENT APPLICATION NUMBER: US/10/395,032  
; CURRENT FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 2736  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: Protocadherin cell adhesion recognition sequence  
US-10-395-032-2736

Query Match 60.8%; Score 31; DB 15; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8  
|:|:|  
Db 1 C1NRDNGC 8

RESULT 6  
US-10-006-869-1084  
; Sequence 1084, Application US/10006869  
; Publication No. US20030082166A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C7  
; CURRENT APPLICATION NUMBER: US/10/006,869  
; CURRENT FILING DATE: 2001-12-03  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1084  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-10-006-869-1084

Query Match 58.8%; Score 30; DB 14; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8  
|:|:|  
Db 1 C1DSGNGC 8

RESULT 7  
US-10-395-032-1084  
; Sequence 1084, Application US/10395032  
; Publication No. US20030229199A1  
; GENERAL INFORMATION:  
; APPLICANT: Blaschuk, Orest W.  
; APPLICANT: Symonds, James Matthew  
; APPLICANT: Gour, Barbara J.  
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR MODULATING NONCLASSICAL  
; TITLE OF INVENTION: CADHERIN-MEDIATED FUNCTIONS  
; FILE REFERENCE: 100086.407C9  
; CURRENT APPLICATION NUMBER: US/10/395,032  
; CURRENT FILING DATE: 2003-03-21  
; NUMBER OF SEQ ID NOS: 4052  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 1084  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Representative cyclic modulating agent based on  
; OTHER INFORMATION: cadherin-6 cell adhesion recognition sequence  
US-10-395-032-1084

Query Match 58.8%; Score 30; DB 15; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8  
|:|:|  
Db 1 C1DSGNGC 8

RESULT 8  
US-10-363-208-97  
; Sequence 97, Application US/10363208  
; Publication No. US20040048243A1  
; GENERAL INFORMATION:  
; APPLICANT: Board of Regents, The University of Texas System  
; TITLE OF INVENTION: Methods and Compositions for In Vitro Targeting  
; FILE REFERENCE: 005774.P005PCT  
; CURRENT APPLICATION NUMBER: US/10/363,208  
; CURRENT FILING DATE: 2003-03-07  
; NUMBER OF SEQ ID NOS: 273  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 97  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; NAME/KEY: Peptide  
; LOCATION: (1)..(8)  
; OTHER INFORMATION: synthetic construct  
US-10-363-208-97

Query Match 58.8%; Score 30; DB 15; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8  
|:|:|  
Db 1 C1WRGSGC 8

RESULT 9  
 US-10-838-289-297  
 ; Sequence 297, Application US/10838289  
 ; Publication No. US20050058603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gao, Jinming  
 ; APPLICANT: Ai, Hua  
 ; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
 ; TITLE OF INVENTION: NANOSHELLS  
 ; FILE REFERENCE: CWRU-P01-040  
 ; CURRENT APPLICATION NUMBER: US/10/838,289  
 ; CURRENT FILING DATE: 2004-05-03  
 ; PRIOR APPLICATION NUMBER: US 60/502,429  
 ; PRIOR FILING DATE: 2003-09-12  
 ; PRIOR APPLICATION NUMBER: US 60/467,389  
 ; PRIOR FILING DATE: 2003-05-02  
 ; NUMBER OF SEQ ID NOS: 756  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 297  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Retina homing peptide  
 US-10-838-289-297

Query Match 58.8%; Score 30; DB 17; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
 | : ||:|  
 Db 1 CMSLGNNC 8

RESULT 10  
 US-10-363-205-130  
 ; Sequence 130, Application US/10363205  
 ; Publication No. US20050074747A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Board of Regents, The University of Texas System  
 ; TITLE OF INVENTION: Biopanning and Rapid Analysis of Selective Interactive Ligands (B  
 ; FILE REFERENCE: 005774.P004PCT  
 ; CURRENT APPLICATION NUMBER: US/10/363,205  
 ; CURRENT FILING DATE: 2003-03-07  
 ; NUMBER OF SEQ ID NOS: 289  
 ; SOFTWARE: PatentIn version 3.1  
 ; SEQ ID NO 130  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; NAME/KEY: Peptide  
 ; LOCATION: (1)..(8)  
 ; OTHER INFORMATION: synthetic construct  
 US-10-363-205-130

Query Match 58.8%; Score 30; DB 17; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
 | : ||:|  
 Db 1 CSYKANSK 8

RESULT 11  
 US-10-607-595-240  
 ; Sequence 240, Application US/10607595  
 ; Publication No. US20050074812A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruoslahti, Erkki  
 ; APPLICANT: Pasqualini, Renata

; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
 ; TITLE OF INVENTION: Tissues  
 ; FILE REFERENCE: P-LJ 4514  
 ; CURRENT APPLICATION NUMBER: US/10/607,595  
 ; CURRENT FILING DATE: 2003-06-27  
 ; PRIOR APPLICATION NUMBER: US/09/722,250  
 ; PRIOR FILING DATE: 2000-11-22  
 ; PRIOR APPLICATION NUMBER: US 09/042,107  
 ; PRIOR FILING DATE: 1998-03-13  
 ; NUMBER OF SEQ ID NOS: 437  
 ; SOFTWARE: PatentIn Ver. 2.0  
 ; SEQ ID NO 240  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Artificial Sequence  
 ; FEATURE:  
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
 US-10-607-595-240

Query Match 58.8%; Score 30; DB 17; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
 | : ||:|  
 Db 1 CMSLGNNC 8

RESULT 12  
 US-10-838-289-136  
 ; Sequence 136, Application US/10838289  
 ; Publication No. US20050058603A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gao, Jinming  
 ; APPLICANT: Ai, Hua  
 ; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
 ; TITLE OF INVENTION: NANOSHELLS  
 ; FILE REFERENCE: CWRU-P01-040  
 ; CURRENT APPLICATION NUMBER: US/10/838,289  
 ; CURRENT FILING DATE: 2004-05-03  
 ; PRIOR APPLICATION NUMBER: US 60/502,429  
 ; PRIOR FILING DATE: 2003-09-12  
 ; PRIOR APPLICATION NUMBER: US 60/467,389  
 ; PRIOR FILING DATE: 2003-05-02  
 ; NUMBER OF SEQ ID NOS: 756  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 136  
 ; LENGTH: 8  
 ; TYPE: PRT  
 ; ORGANISM: Unknown  
 ; FEATURE:  
 ; OTHER INFORMATION: Lung homing peptide  
 US-10-838-289-136

Query Match 56.9%; Score 29; DB 17; Length 8;  
 Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CLHRGNSC 8  
 | : ||:|  
 Db 1 CRHESSSC 8

RESULT 13  
 US-10-607-595-33  
 ; Sequence 33, Application US/10607595  
 ; Publication No. US20050074812A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Ruoslahti, Erkki  
 ; APPLICANT: Pasqualini, Renata  
 ; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
 ; TITLE OF INVENTION: Tissues  
 ; FILE REFERENCE: P-LJ 4514

; CURRENT APPLICATION NUMBER: US/10/607,595  
; CURRENT FILING DATE: 2003-06-27  
; PRIOR APPLICATION NUMBER: US/09/722,250  
; PRIOR FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: US 09/042,107  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 437  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 33  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-10-607-595-33

Query Match 56.9%; Score 29; DB 17; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8  
| | | | |  
Db 1 CRHESSC 8

RESULT 14  
US-10-433-452A-9  
; Sequence 9, Application US/10433452A  
; Publication No. US20040101905A1  
; GENERAL INFORMATION:  
; APPLICANT: Brekke, Ole Henrik  
; APPLICANT: Lauvrak, Vigdis  
; APPLICANT: Sandlie, Inger  
; TITLE OF INVENTION: Hybrid Antibodies  
; FILE REFERENCE: DEH-0014  
; CURRENT APPLICATION NUMBER: US/10/433,452A  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: GB 0029407.4  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 58  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Fc effector peptide  
US-10-433-452A-9

Query Match 54.9%; Score 28; DB 16; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8  
| | | | |  
Db 1 CLRSGGC 8

RESULT 15  
US-10-433-452A-10  
; Sequence 10, Application US/10433452A  
; Publication No. US20040101905A1  
; GENERAL INFORMATION:  
; APPLICANT: Brekke, Ole Henrik  
; APPLICANT: Lauvrak, Vigdis  
; APPLICANT: Sandlie, Inger  
; TITLE OF INVENTION: Hybrid Antibodies  
; FILE REFERENCE: DEH-0014  
; CURRENT APPLICATION NUMBER: US/10/433,452A  
; CURRENT FILING DATE: 2003-11-24  
; PRIOR APPLICATION NUMBER: GB 0029407.4  
; PRIOR FILING DATE: 2000-12-01  
; NUMBER OF SEQ ID NOS: 58

; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 10  
; LENGTH: 8  
; TYPE: PRT  
; ORGANISM: Artificial  
; FEATURE:  
; OTHER INFORMATION: Fc effector peptide  
US-10-433-452A-10

Query Match 54.9%; Score 28; DB 16; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 CLHRGNSC 8  
| | | | |  
Db 1 CLRSGGC 8

Search completed: August 3, 2005, 12:32:58  
Job time : 151 secs

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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:29:24 ; Search time 38 Seconds  
(without alignments)  
30.384 Million cell updates/sec

Title: US-09-910-582B-10

Perfect score: 74

Sequence: 1 CRSWNKADNRSC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 1582

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 79:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	25	33.8	10	2 PH0923	T-cell receptor be
2	22	29.7	5	2 JH0253	gut pentapeptide -
3	20	27.0	11	2 S32575	ribosomal protein
4	20	27.0	12	2 S51737	T-cell receptor be
5	20	27.0	12	2 B49033	T-cell receptor de
6	19	25.7	8	2 S19288	acylase - Kluyvera
7	19	25.7	10	2 A35556	hypothetical prote
8	19	25.7	10	2 S23370	T-cell receptor al
9	19	25.7	10	2 F49033	T-cell receptor ga
10	19	25.7	10	2 C41946	T-cell receptor ga
11	19	25.7	11	2 PH1376	T antigen variant
12	19	25.7	12	2 S36902	Em protein - wheat
13	18	24.3	8	2 S59622	metallothionein is
14	18	24.3	8	2 C61512	variant surface gl
15	18	24.3	8	2 I57018	gene cfr protein
16	18	24.3	9	2 PT0272	Ig heavy chain CRD
17	18	24.3	11	2 I41946	T-cell receptor ga
18	18	24.3	11	2 PH0903	T-cell receptor be
19	17	23.0	6	2 F41946	T-cell receptor ga
20	17	23.0	8	2 S70727	lpf protein - shi
21	17	23.0	8	2 A38887	T-cell receptor ga
22	17	23.0	8	2 A39308	glycine reductase
23	17	23.0	8	2 A41117	acetylcholinestera
24	17	23.0	10	2 JCL167	thyroliberin poten
25	17	23.0	10	2 B49033	T-cell receptor ga
26	17	23.0	10	2 B41946	T-cell receptor ga
27	17	23.0	11	2 D41946	T-cell receptor ga
28	17	23.0	11	2 B41946	T-cell receptor ga
29	17	23.0	11	2 C38887	T-cell receptor ga

30	17	23.0	11	2 A49037	TCR gamma V-J regi
31	17	23.0	11	2 B49037	TCR gamma V-J regi
32	17	23.0	11	2 C49037	TCR gamma V-J regi
33	17	23.0	11	2 S45698	gamma-MSH-like pro
34	17	23.0	12	2 PH1308	Ig heavy chain DJ
35	17	23.0	12	2 S25039	Ig heavy chain V r
36	16	21.6	5	2 PT0580	T-cell receptor be
37	16	21.6	7	4 I55382	hypothetical pepti
38	16	21.6	9	2 PT0299	Ig heavy chain CRD
39	16	21.6	9	2 PH0943	T-cell receptor be
40	16	21.6	10	2 S15118	dihydrofolate redu
41	16	21.6	10	2 S63696	DNA polymerase - y
42	16	21.6	10	2 PT0310	Ig heavy chain CRD
43	16	21.6	10	2 PH0807	T-cell receptor al
44	16	21.6	11	2 A34662	Achatina cardio-ex
45	16	21.6	11	2 S05002	corazonin - Americ
46	16	21.6	12	2 S26548	T-cell receptor be
47	16	21.6	12	2 S26553	T-cell receptor be
48	16	21.6	12	2 A49033	T-cell receptor de
49	15	20.3	4	2 PT0661	T-cell receptor be
50	15	20.3	5	2 PT0695	T-cell receptor be
51	15	20.3	6	2 A31263	dihydrofolate redu
52	15	20.3	6	2 B35840	cerebellar degener
53	15	20.3	6	2 A61068	locustakinin - mig
54	15	20.3	7	2 S38516	mablin II chain
55	15	20.3	7	2 PN0649	pullulanase (EC 3.
56	15	20.3	7	2 S57274	triacylglycerol li
57	15	20.3	7	2 A61081	tryptophyllin, bas
58	15	20.3	8	2 S10596	adipokinetic hormo
59	15	20.3	8	2 JS0315	leucokinin V - Mad
60	15	20.3	8	2 JS0316	leucokinin VI - Ma
61	15	20.3	8	2 JS0317	leucokinin VII - M
62	15	20.3	8	2 JS0318	leucokinin VIII -
63	15	20.3	8	2 A28495	conopressin G - co
64	15	20.3	9	2 B28495	conopressin S - co
65	15	20.3	9	2 A24244	adipokinetic hormo
66	15	20.3	9	2 JS0302	xenopsin-related p
67	15	20.3	9	2 A60320	xenopsin-related p
68	15	20.3	9	2 I58350	gene c-mpl protein
69	15	20.3	9	2 PH0921	T-cell receptor be
70	15	20.3	9	2 S39040	lysine-conopressin
71	15	20.3	9	2 PC2021	oxytocin-related p
72	15	20.3	9	2 D57444	neuropeptide Grb-A
73	15	20.3	9	2 B45020	probable minipolyp
74	15	20.3	10	2 C39191	hypothetical prote
75	15	20.3	10	2 PT0322	Ig heavy chain CRD
76	15	20.3	10	2 B38887	T-cell receptor ga
77	15	20.3	10	2 A59272	peptide-N4-(N-acet
78	15	20.3	10	2 H37196	bradykinin-potenti
79	15	20.3	10	2 S53789	neuropeptide Pec-H
80	15	20.3	11	2 S66196	alcohol dehydrogen
81	15	20.3	11	2 S04875	mfs protein - Bra
82	15	20.3	11	2 S70338	napin small chain
83	15	20.3	11	2 S68637	acetylcholinestera
84	15	20.3	12	2 PH1675	Ig heavy chain V r
85	15	20.3	12	2 PT0274	Ig heavy chain CRD
86	15	20.3	12	2 PH1324	Ig heavy chain DJ
87	15	20.3	12	2 H41946	T-cell receptor ga
88	15	20.3	12	2 I41235	glutamine-tRNA lig
89	15	20.3	12	2 S29859	gene p10 protein -
90	15	20.3	12	2 I75529	estrogen receptor
91	14	18.9	7	2 PT0576	T-cell receptor be
92	14	18.9	8	2 A37521	R-phycocerythrin ga
93	14	18.9	9	2 S78426	S2.5K protein - sp
94	14	18.9	10	2 A40753	aldehyde ferredoxi
95	14	18.9	11	2 B43669	hypothetical prote
96	14	18.9	11	2 T06383	hypothetical prote
97	14	18.9	11	2 PT0249	Ig heavy chain CRD
98	14	18.9	11	2 PH1375	T antigen variant
99	14	18.9	11	2 PQ0731	unidentified 5.7/3
100	14	18.9	11	2 S23926	major glycoprotein

## ALIGNMENTS

RESULT 1  
PH0923  
T-cell receptor beta chain V-D-J region (isolate 9) - rat (fragment)  
C;Species: Rattus norvegicus (Norway rat)  
C;Date: 09-Oct-1992 #sequence\_revision 09-Oct-1992 #text\_change 30-May-1997  
C;Accession: PH0923  
R;Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.  
J. Exp. Med. 174, 1467-1476, 1991  
A;Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergic  
A;Reference number: PH0991; MUID:92078857; PMID:1836012  
A;Accession: PH0923  
A;Molecule type: mRNA  
A;Residues: 1-10 <GO>  
A;Experimental source: concanavalin A-activated lymphoblast  
C;Keywords: T-cell receptor

Query Match 33.8%; Score 25; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 3.8e+02; Indels 0; Gaps 0;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSWNK 6  
| | | :  
Db 1 CASNGR 6

RESULT 2  
JH0253  
gut pentapeptide - Japanese eel  
C;Species: Anguilla japonica (Japanese eel)  
C;Date: 31-Mar-1992 #sequence\_revision 31-Mar-1992 #text\_change 11-Apr-1995  
C;Accession: JH0253  
R;Uesaka, T.; Ikeda, T.; Kubota, I.; Munesaka, Y.; Ando, M.  
Biochem. Biophys. Res. Commun. 180, 828-832, 1991  
A;Title: Structure and function of a pentapeptide isolated from the gut of the eel.  
A;Reference number: JH0253; MUID:92062113; PMID:1953755  
A;Accession: JH0253  
A;Molecule type: protein  
A;Residues: 1-5 <UES>  
A;Experimental source: gut  
C;Comment: This peptide increased basal tone of the circular muscle of the esophagogastric  
, and of the circular muscle of the gastro-intestinal junction.

Query Match 29.7%; Score 22; DB 2; Length 5;  
Best Local Similarity 100.0%; Pred. No. 2.8e+05; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 WNK 6  
| | | :  
Db 3 WNK 5

RESULT 3  
S32575  
ribosomal protein S2, plastid - squawroot plastid (fragment)  
C;Species: plastid Conopholis americana (squawroot)  
C;Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 09-Jul-2004  
C;Accession: S32575  
R;Taylor, G.W.; Wolfe, K.H.; Morden, C.W.; dePamphilis, C.W.; Palmer, J.D.  
Curr. Genet. 20, 515-518, 1991  
A;Title: Lack of a functional plastid tRNA(Cys) gene is associated with loss of photosyn  
A;Reference number: S32575; MUID:92145776; PMID:1723664  
A;Accession: S32575  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-11 <TAY>  
A;Cross-references: UNIPROT:P42341; EMBL:X64567; NID:g11275; PIDN:CAA45868.1; PID:g11276  
C;Genetics:  
A;Gene: rps2  
A;Genome: plastid  
C;Superfamily: Escherichia coli ribosomal protein S2

C;Keywords: plastid; protein biosynthesis; ribosome

Query Match 27.0%; Score 20; DB 2; Length 11;  
Best Local Similarity 75.0%; Pred. No. 2.9e+03; Indels 0; Gaps 0;  
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 RSWN 5

Db 4 RYWN 7

## RESULT 4

S51737

T-cell receptor beta-chain joining region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 07-May-1995 #sequence\_revision 01-Sep-1995 #text\_change 05-Nov-1999

C;Accession: S51737

R;Durinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.

submitted to the EMBL Data Library, November 1993

A;Reference number: S51732

A;Accession: S51737

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-12 &lt;DUR&gt;

A;Cross-references: EMBL:Z28345; NID:g607126; PIDN:CAA82199.1; PID:g607127

C;Keywords: T-cell receptor

Query Match 27.0%; Score 20; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 3.1e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRSWNKAD 8

Db 1 CASSQSEAD 8

## RESULT 5

B49033

T-cell receptor delta chain V-D-J region - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 19-Dec-1993 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000

C;Accession: B49033

R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.

Eur. J. Immunol. 21, 2999-3007, 1991

A;Title: Functionally distinct subsets of human gamma/delta T cells.

A;Reference number: A49033; MUID:92083926; PMID:1684157

A;Accession: B49033

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-12 &lt;MOR&gt;

A;Cross-references: GB:S72580; NID:g240692; PIDN:AAB20628.1; PID:g240693

A;Note: sequence extracted from NCBI backbone (NCBIN:72580, NCBI:P:72582)

C;Keywords: T-cell receptor

Query Match 27.0%; Score 20; DB 2; Length 12;

Best Local Similarity 28.6%; Pred. No. 3.1e+03;

Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRSWNKA 7

Db 3 CDTWGSS 9

## RESULT 6

S19288

acylase - Kluyvera cryocrescens

C;Species: Kluyvera cryocrescens

C;Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 09-Jul-2004

C;Accession: S19288

R;Martin, J.; Slade, A.; Aitken, A.; Arche, R.; Virden, R.

Biochem. J. 280, 659-662, 1991

A;Title: Chemical modification of serine at the active site of penicillin acylase from KJ

A;Reference number: S19288; MUID:92109664; PMID:1764029



A;Accession: S19288  
A;Status: preliminary  
A;Molecule type: protein  
A;Residues: 1-8 <MAR>  
A;Cross-references: UNIPROT:Q7M124

Query Match 25.7%; Score 19; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 2.8e+05;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSW 4  
| : |  
Db 1 CNMW 4

## RESULT 7

A35556  
hypothetical protein (ODC region) - human  
C;Species: Homo sapiens (man)  
C;Date: 21-Sep-1990 #sequence\_revision 21-Sep-1990 #text\_change 30-Sep-1993  
C;Accession: A35556  
R;Moshier, J.A.; Gilbert, J.D.; Skunca, M.; Donescu, J.; Almodovar, K.M.; Luk, G.D.  
J. Biol. Chem. 265, 4884-4892, 1990  
A;Title: Isolation and expression of a human ornithine decarboxylase gene.  
A;Reference number: A35556; MUID:90202959; PMID:2318872  
A;Accession: A35556  
A;Status: preliminary; not compared with conceptual translation  
A;Molecule type: DNA  
A;Residues: 1-10 <MOS>  
A;Cross-references: GB:J05271

Query Match 25.7%; Score 19; DB 2; Length 10;  
Best Local Similarity 50.0%; Pred. No. 3.8e+03;  
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 CRSW 4  
| : |  
Db 5 CGAW 8

## RESULT 8

S23370  
T-cell receptor alpha chain J region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 22-Nov-1993 #sequence\_revision 26-May-1995 #text\_change 17-Mar-1999  
C;Accession: S23370  
R;Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichman  
Eur. J. Immunol. 21, 2749-2754, 1991  
A;Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rheu  
A;Reference number: S23364; MUID:92037820; PMID:1657615  
A;Accession: S23370  
A;Status: preliminary; translation not shown  
A;Molecule type: mRNA  
A;Residues: 1-10 <PLU>  
A;Cross-references: EMBL:X58165  
C;Keywords: T-cell receptor

Query Match 25.7%; Score 19; DB 2; Length 10;  
Best Local Similarity 42.9%; Pred. No. 3.8e+03;  
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WNKADNR 10  
| : | : |  
Db 3 WDNDNMR 9

## RESULT 9

F49033  
T-cell receptor gamma chain V-D-J region - human (fragment)  
C;Species: Homo sapiens (man)  
C;Date: 19-Dec-1993 #sequence\_revision 17-Mar-2000 #text\_change 17-Mar-2000  
C;Accession: F49033  
R;Morita, C.T.; Verma, S.; Aparicio, P.; Martinez, C.; Spits, H.; Brenner, M.B.

Eur. J. Immunol. 21, 2999-3007, 1991

A;Title: Functionally distinct subsets of human gamma/delta T cells.

A;Reference number: A49033; MUID:92083926; PMID:1684157

A;Accession: F49033

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-10 <MOR>

A;Cross-references: GB:S72605; NID:G240700; PIDN:AAB20632.1; PID:G240701

A;Note: sequence extracted from NCBI backbone (NCBIN:72605, NCBI:P:72606)

C;Keywords: T-cell receptor

Query Match 25.7%; Score 19; DB 2; Length 10;  
Best Local Similarity 33.3%; Pred. No. 3.8e+03;  
Matches 2; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRSWNK 6  
| : |  
Db 1 CALWER 6

## RESULT 10

C41946  
T-cell receptor gamma chain (1t.60) - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 03-Feb-1994 #sequence\_revision 03-Feb-1994 #text\_change 07-May-1999  
C;Accession: C41946  
R;Whetsell, M.; Mosley, R.L.; Whetsell, L.; Schaefer, F.V.; Miller, K.S.; Klein, J.R.  
Mol. Cell. Biol. 11, 5902-5909, 1991

A;Title: Rearrangement and junctional-site sequence analyses of T-cell receptor gamma ge  
A;Reference number: A41946; MUID:92049316; PMID:1658619

A;Accession: C41946

A;Status: preliminary; not compared with conceptual translation

A;Molecule type: DNA

A;Residues: 1-10 <WHE>

C;Keywords: T-cell receptor

Query Match 25.7%; Score 19; DB 2; Length 10;  
Best Local Similarity 28.6%; Pred. No. 3.8e+03;  
Matches 2; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 CRSWNKA 7  
| : | : |  
Db 2 CAVWSSS 8

## RESULT 11

PH1376  
T antigen variant K-3 - mouse (fragment)  
C;Species: Mus musculus (house mouse)  
C;Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000  
C;Accession: PH1376  
R;Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.  
J. Exp. Med. 176, 449-457, 1992  
A;Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for tra  
A;Reference number: PH1373; MUID:92364547; PMID:1380062

A;Accession: PH1376

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-11 <Lil>

Query Match 25.7%; Score 19; DB 2; Length 11;  
Best Local Similarity 50.0%; Pred. No. 4.2e+03;  
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSWNK 6  
| : | : |  
Db 1 CKGVNK 6

## RESULT 12

S36902  
Em protein - wheat (fragment)  
C;Species: Triticum sp. (wheat)

C;Date: 04-Mar-1994 #sequence\_revision 19-Jul-1996 #text\_change 09-Jul-2004

C;Accession: S36902  
 R;Taylor, R.M.; Cumming, A.C.  
 FEBS Lett. 331, 76-80, 1993  
 A;Title: Purification of an endoproteinase that digests the wheat 'Em' protein in vitro,  
 A;Reference number: S36902; MUID:94009650; PMID:8405415  
 A;Accession: S36902  
 A;Molecule type: protein  
 A;Residues: 1-12 <TA>  
 A;Cross-references: UNIPROT:Q7M272  
 C;Superfamily: embryonic abundant protein Em

Query Match 25.7%; Score 19; DB 2; Length 12;  
 Best Local Similarity 57.1%; Pred. No. 4.5e+03;  
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 NKADNRS 11  
 : : :  
 Db 4 NLAEGRS 10

## RESULT 13

S59622  
 metallothionein isoform a, cadmium-binding - Arianta arbustorum (terrestrial snail) (fra  
 C;Species: Arianta arbustorum  
 C;Date: 19-Mar-1997 #sequence\_revision 24-Oct-1997 #text\_change 09-Jul-2004  
 R;Accession: S59622  
 R;Berger, B.; Hunziker, P.E.; Hauer, C.R.; Birchler, N.; Dallinger, R.  
 Biochem. J. 311, 951-957, 1995  
 A;Title: Mass spectrometry and amino acid sequencing of two cadmium-binding metallothion  
 A;Reference number: S59621; MUID:96067616; PMID:7487956  
 A;Accession: S59622  
 A;Molecule type: protein  
 A;Residues: 1-8 <BER>  
 A;Cross-references: UNIPROT:P55946  
 C;Superfamily: metallothionein  
 C;Keywords: chelation; metal binding; metal-thiolate cluster

Query Match 24.3%; Score 18; DB 2; Length 8;  
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 NRSC 12  
 : : :  
 Db 2 NSSC 5

## RESULT 14

C61512  
 variant surface glycoprotein MITat 1.4 - Trypanosoma brucei (fragment)  
 C;Species: Trypanosoma brucei  
 C;Date: 28-Oct-1994 #sequence\_revision 28-Oct-1994 #text\_change 09-Jul-2004  
 C;Accession: C61512  
 R;Holder, A.A.; Cross, G.A.M.  
 Mol. Biochem. Parasitol. 2, 135-150, 1981  
 A;Title: Glycopeptides from variant surface glycoproteins of Trypanosoma brucei. C-termi  
 A;Reference number: A61512; MUID:81172836; PMID:6163983  
 A;Accession: C61512  
 A;Status: preliminary  
 A;Molecule type: protein  
 A;Residues: 1-8 <HOL>  
 A;Cross-references: UNIPROT:Q7M3S3  
 C;Keywords: glycoprotein

Query Match 24.3%; Score 18; DB 2; Length 8;  
 Best Local Similarity 40.0%; Pred. No. 2.8e+05;  
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 DNRSC 12  
 : : :  
 Db 2 ENNAC 6

## RESULT 15

I57018  
 gene Cfr protein - mouse (fragment)  
 C;Species: Mus sp. (mouse)  
 C;Date: 02-Aug-1996 #sequence\_revision 02-Aug-1996 #text\_change 09-Jul-2004  
 C;Accession: I57018  
 R;Dorin, J.R.; Stevenson, B.J.; Fleming, S.; Alton, E.W.; Dickinson, P.; Porteous, D.J.  
 Mamm. Genome 5, 465-472, 1994  
 A;Title: Long-term survival of the exon 10 insertional cystic fibrosis mutant mouse is a  
 A;Reference number: I57018; MUID:95037043; PMID:7949729  
 A;Accession: I57018  
 A;Status: preliminary; translated from GB/EMBL/DDBJ  
 A;Molecule type: DNA  
 A;Residues: 1-8 <RES>  
 A;Cross-references: UNIPROT:Q7M056; GB:S74246; NID:g710482  
 C;Genetics:  
 A;Gene: Cfr

Query Match 24.3%; Score 18; DB 2; Length 8;  
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;  
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DNRSC 12  
 : : :  
 Db 3 DSPSC 7

Search completed: August 3, 2005, 12:40:39  
 Job time : 39 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:21:19 ; Search time 165 Seconds  
(without alignments)  
37.242 Million cell updates/sec

Title: US-09-910-582B-10  
Perfect score: 74  
Sequence: 1 CRSWNKADNRSC 12

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues  
Total number of hits satisfying chosen parameters: 4233

Minimum DB seq length: 0  
Maximum DB seq length: 12

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : Uniprot\_03:\*  
1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	22	29.7	12	2	Q93WB7
2	21	28.4	9	2	O71066
3	21	28.4	10	2	Q6LDE2
4	21	28.4	11	2	Q6DW13
5	21	28.4	12	2	Q93WF2
6	21	28.4	12	2	Q9QVF2
7	20	27.0	11	1	RR2_CONAM
8	20	27.0	11	2	Q9T019
9	20	27.0	12	2	Q86CU1
10	20	27.0	12	2	Q86FU4
11	20	27.0	12	2	Q9ZAM7
12	19	25.7	8	2	Q70Y84
13	19	25.7	8	2	Q7M124
14	19	25.7	10	2	Q6LBT3
15	19	25.7	11	2	Q77908
16	19	25.7	12	2	Q9BP48
17	19	25.7	12	2	Q7M272
18	19	25.7	12	2	Q6LEB4
19	18	24.3	8	2	Q7M3S3
20	18	24.3	8	2	Q7M056
21	18	24.3	8	2	Q9DSN4
22	18	24.3	8	2	Q9DSN5
23	18	24.3	8	2	Q9E8P8
24	18	24.3	8	2	Q9E8P9
25	18	24.3	8	2	Q9E8Q0
26	18	24.3	8	2	Q9E8Q1
27	18	24.3	8	2	Q9E8Q4
28	18	24.3	8	2	Q9E8Q5
29	18	24.3	8	2	Q9E8Q6
30	18	24.3	8	2	Q9E8Q7
31	18	24.3	9	1	NEF_HV1Z8

ALIGNMENTS

32	18	24.3	9	2	Q7KYP6	Q7kyp6 homo sapien
33	18	24.3	9	2	Q9UCQ9	Q9ucq9 homo sapien
34	18	24.3	9	2	Q6XBN2	Q6xbn2 vitta pach
35	18	24.3	9	2	Q85G96	Q85g96 pyrrhobryum
36	18	24.3	9	2	Q6VCX0	Q6vcx0 streptomyce
37	18	24.3	9	2	Q9RE35	Q9re35 chlamydia t
38	18	24.3	10	1	SP34_DICMU	SP34 dictyosteli
39	18	24.3	10	2	Q71GZ2	Q71gz2 andrena lim
40	18	24.3	10	2	Q8SAC2	Q8sac2 amblystegiu
41	18	24.3	10	2	Q847B5	Q847b5 bacillus am
42	18	24.3	11	1	LADD_ONCMY	LADD oncorhynchu
43	18	24.3	11	2	Q35374	Q35374 paramecium
44	18	24.3	11	2	Q6W928	Q6w928 candidatus
45	18	24.3	12	1	RS19_TOBBP	RS19 tomato big
46	18	24.3	12	2	Q96PK0	Q96pk0 homo sapien
47	18	24.3	12	2	Q9H1Z6	Q9h1z6 homo sapien
48	18	24.3	12	2	Q41611	Q41611 human immun
49	17	23.0	8	2	Q71VP0	Q71vp0 ovis aries
50	17	23.0	8	2	Q85406	Q85406 coxiella bu
51	17	23.0	8	2	Q6LAA8	Q6laa8 shigella fl
52	17	23.0	8	2	Q7M0L0	Q7m0l0 clostridium
53	17	23.0	8	2	Q98TU5	Q98tu5 xenopus lae
54	17	23.0	8	2	Q7LZ27	Q7lzt7 raja oxiata
55	17	23.0	10	1	AKHX_LOCMI	AKHX locusta mig
56	17	23.0	10	1	NO40_TOBAC	NO40 nicotiana t
57	17	23.0	10	2	Q7M2Z8	Q7m2z8 bos taurus
58	17	23.0	10	2	Q9TR47	Q9tr47 bos taurus
59	17	23.0	10	2	Q70Y78	Q70y78 plectranthu
60	17	23.0	10	2	Q947R7	Q947r7 solanum tub
61	17	23.0	10	2	Q6TS30	Q6ts30 lycopersico
62	17	23.0	10	2	Q8JFE7	Q8jfe7 ficedula al
63	17	23.0	10	2	Q8J333	Q8j333 ficedula hy
64	17	23.0	10	2	Q9PRU9	Q9pru9 sparus aura
65	17	23.0	11	1	MLG_THETS	MLG thernomyzon
66	17	23.0	11	2	Q60761	Q60761 homo sapien
67	17	23.0	12	1	NO40_LOTJA	NO40 lotus japon
68	17	23.0	12	1	NO40_SESRO	NO40 sesbania ro
69	17	23.0	12	2	P92454	P92454 cycas revol
70	17	23.0	12	2	Q37071	Q37071 petunia hyb
71	17	23.0	12	2	Q8LLC3	Q8llc3 trifolium r
72	17	23.0	12	2	Q75729	Q75729 human immun
73	16	21.6	4	1	QCP3_OCTMI	QCP3 octopus min
74	16	21.6	8	2	Q64971	Q64971 alfalfa mos
75	16	21.6	9	2	Q6Z200	Q6z200 silene rotu
76	16	21.6	9	2	Q6LAQ1	Q6lad1 rattus norv
77	16	21.6	9	2	O12096	O12096 caprine art
78	16	21.6	9	2	O12098	O12098 caprine art
79	16	21.6	9	2	O12100	O12100 caprine art
80	16	21.6	9	2	O12102	O12102 caprine art
81	16	21.6	9	2	O12104	O12104 caprine art
82	16	21.6	10	1	MP2_MICOC	MP2 microplitis
83	16	21.6	10	2	Q15342	Q15342 homo sapien
84	16	21.6	10	2	Q6M69	Q6m69 potato viru
85	16	21.6	10	2	Q8UT83	Q8ut83 human immun
86	16	21.6	11	1	CEP1_ACHFU	CEP1 achatina fu
87	16	21.6	11	1	COR2_PERAM	COR2 periplaneta
88	16	21.6	11	2	Q77914	Q77914 oreochromis
89	16	21.6	11	2	Q78118	Q78118 oreochromis
90	16	21.6	11	2	Q78120	Q78120 oreochromis
91	16	21.6	11	2	Q6LD68	Q6ld68 mus sp. acu
92	16	21.6	11	2	Q8CGW6	Q8cgw6 rattus norv
93	16	21.6	12	2	Q9BZ49	Q9bz49 homo sapien
94	16	21.6	12	2	Q77889	Q77889 oreochromis
95	16	21.6	12	2	Q77890	Q77890 oreochromis
96	16	21.6	12	2	Q77891	Q77891 oreochromis
97	16	21.6	12	2	Q77920	Q77920 pseudotroph
98	16	21.6	12	2	O12074	O12074 caprine art
99	16	21.6	12	2	O12076	O12076 caprine art
100	16	21.6	12	2	O12078	O12078 caprine art

```

RESULT 1
Q93WB7 ID Q93WB7 PRELIMINARY; PRT; 12 AA.
AC Q93WB7;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early nodulin.
GN Name=ENOD40C;
OS Lupinus luteus (Yellow lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genistaceae; Lupinus.
OX NCBI_TaxID=3873;
RN [1]
RN SEQUENCE FROM N.A.
RP Podkowinski J., Grabowska B., Kisiel A., Dlugaszewska B.,
RA Nimmagadda G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Podkowinski J., Kisiel A., Grabowska B., Dlugaszewska B.,
RA Nimmagadda G.;
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF352374; AAK51421.1; -.
DR EMBL; AF352373; AAK51420.1; -.
SQ SEQUENCE 12 AA; 1439 MW; 383850887CB326C3 CRC64;

Query Match 29.7%; Score 22; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.9e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 WNKADNRS 11
| | | |
DB 5 WOKSINGS 12

RESULT 2
O71066 ID O71066 PRELIMINARY; PRT; 9 AA.
AC O71066;
DT 01-AUG-1998 (TrEMBLrel. 07, Created)
DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Fusion protein (fragment).
OS Canine distemper virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Paramyxoviridae; Paramyxovirinae; Morbillivirus.
OX NCBI_TaxID=11232;
RN [1]
RN SEQUENCE FROM N.A.
RA Liermann H., Harder T., Haas L.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF026234; AAC09164.1; -.
FT NON TER 9
SQ SEQUENCE 9 AA; 1124 MW; F29D045760440441 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.6e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 NKADNRS 11
| | | |
DB 3 NRIPNRS 9

RESULT 3
Q6LDE2 ID Q6LDE2 PRELIMINARY; PRT; 10 AA.
AC Q6LDE2;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Proacrosin protein (Fragment).
GN Name=proacrosin;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE=92331659; PubMed=1628652;
RA Vazquez-Levin M.H., Reventos J., Gordon J.W.;
RT "Molecular cloning, sequencing and restriction mapping of the genomic
RT sequence encoding human proacrosin.";
RL Eur. J. Biochem. 207:23-26(1992).
DR EMBL; S40014; AAD13819.1; -.
FT NON TER 10
SQ SEQUENCE 10 AA; 1007 MW; C26972D44AA33DC2 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 7.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DNRSC 12
| | | |
DB 6 DNATC 10

RESULT 4
Q6DW13 ID Q6DW13 PRELIMINARY; PRT; 11 AA.
AC Q6DW13;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE Cathepsin B (Fragment).
GN Name=CTSB;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RN SEQUENCE FROM N.A.
RA Juszcuk-Kubiak E., Rosochaacki S., Szreder T., Wicinska K.;
RL Submitted (MAY-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY639598; AAT58218.1; -.
FT NON TER 11
FT NON TER 11
SQ SEQUENCE 11 AA; 1265 MW; 39C909F87AB1A453 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 SWN 5
| | | |
DB 3 SWN 5

RESULT 5
Q93WF2 ID Q93WF2 PRELIMINARY; PRT; 12 AA.
AC Q93WF2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Early nodulin.
GN Name=ENOD40B;
OS Lupinus luteus (Yellow lupine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids I; Fabales; Fabaceae; Papilionoideae; Genistaceae; Lupinus.
OX NCBI_TaxID=3873;

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RN [1]
RP SEQUENCE FROM N.A.
RA Podkowinski J., Grabowska B., Kisiel A., Dlugaszewska B.,
RL Nimmagadda G.,
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Kisiel A., Grabowska B., Dlugaszewska B., Nimmagadda G.,
RL Podkowinski J.,
RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF352375; AAK51422.1; -
DR EMBL: AF352372; AAK51419.1; -
SQ SEQUENCE 12 AA; 1403 MW; 283958AE7CB326C3 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 8.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 SWNKA 7
Db |||
4 SWQKS 8

RESULT 6
Q9QVF2 PRELIMINARY; PRT; 12 AA.
ID AC Q9QVF2;
AC Q9QVF2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE TRANSFERRIN-PEPTIDE 21 (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE.
RX MEDLINE=92165927; PubMed=1791188;
RA Cavanaugh P.G., Nicolson G.L.;
RT "Lung-derived growth factor that stimulates the growth of lung-
RT metastasizing tumor cells: identification as transferrin.";
RL J. Cell. Biochem. 47:261-271(1991).
FT NON TER 1
FT NON TER 12
FT NON TER 12
SQ SEQUENCE 12 AA; 1436 MW; 40AD1DFA420AADD3 CRC64;

Query Match 28.4%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 8.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 5 NKAD 8
Db |||
4 NKAD 7

RESULT 7
RP2_CONAM STANDARD; PRT; 11 AA.
ID - RP2_CONAM
AC P42341;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Plastid 30S ribosomal protein S2 (Fragment).
GN Name=rp2;
OS Conopholis americana (Squawroot).
OG Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiaceae; Orobanchaceae; Orobanchaceae; Conopholis.
OX NCBI_TaxID=41179;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=92145776; PubMed=1723664;

Taylor G., Wolfe K.H., Morden C.W., Depamphilis C.W., Palmer J.D.;
RT "Lack of a functional plastid trnA(Cys) gene is associated with loss
of photosynthesis in a lineage of parasitic plants.";
Curr. Genet. 20:515-518(1991).
CC -1- SUBCELLULAR LOCATION: Plastid
CC -1- SIMILARITY: Belongs to the ribosomal protein S2P family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL Outstation -
the European Bioinformatics Institute. There are no restrictions on its
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entities requires a license agreement (See http://www.isb-sib.ch/announce/
or send an email to license@isb-sib.ch).
EMBL: X64567; CAA45868.1; -
DR PIR: S32575; S32575.
DR HAMAP: MF_00291; -; 1
DR InterPro: IPR001865; Ribosomal_S2.
DR PROSITE: PS00962; RIBOSOMAL_S2_1; PARTIAL.
DR PROSITE: PS00963; RIBOSOMAL_S2_2; PARTIAL.
KW Chloroplast; Ribosomal protein.
FT NON TER 11
FT NON TER 11
SQ SEQUENCE 11 AA; 1497 MW; 76CD719954536B44 CRC64;

Query Match 27.0%; Score 20; DB 1; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 RSWN 5
Db |||
4 RYWN 7

RESULT 8
Q9TOL9 PRELIMINARY; PRT; 11 AA.
ID AC Q9TOL9
AC Q9TOL9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE SLG5 protein (Fragment).
GN Name=SLG5;
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosid1; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99264316; PubMed=10330480;
RA Cabrilla D., Delorme V., Garin J., Ruffio-Chable V., Giranton J.L.,
RA Dumas C., Gaudé T., Cock J.M.;
RT "The S15 self-incompatibility haplotype in Brassica includes three S
RT gene family members which are expressed in stigmas.";
RL Plant Cell 11:971-986(1999).
RN [2]
RP SEQUENCE FROM N.A.
RA Cock M.J.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: Y18256; CAB41875.1; -
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 11 AA; 1035 MW; CD3806DDA8772AAD CRC64;

Query Match 27.0%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 NKADNRSC 12
Db |||
2 NAADLGTC 9

```

## RESULT 9

Q86CU1 ID Q86CU1 PRELIMINARY; PRT; 12 AA.  
 AC Q86CU1; 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Trypsin 1 (Fragment)  
 GN Name=Try1; Synonyms=try1;  
 OS Drosophila novamexicana.  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=47314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=15010-1031.0;  
 RX MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;  
 RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;  
 RT "Drosophila pigmentation evolution: divergent genotypes underlying  
 convergent phenotypes.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813 (2003).  
 DR EMBL; AY165534; AAP21578.1; -.  
 DR FlyBase; FBgn0066204; Dnov\Try1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 12 AA; 1301 MW; DF5820B9A84452D2 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RSW 4  
 DB 2 RSW 4

## RESULT 10

Q86FU4 ID Q86FU4 PRELIMINARY; PRT; 12 AA.  
 AC Q86FU4; 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Trypsin 1 (Fragment)  
 GN Name=Try1; Synonyms=try1;  
 OS Drosophila americana (Fruit fly).  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=40366;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=15010-0951.0;  
 RX MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;  
 RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;  
 RT "Drosophila pigmentation evolution: divergent genotypes underlying  
 convergent phenotypes.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813 (2003).  
 DR EMBL; AY165534; AAP12724.1; -.  
 DR FlyBase; FBgn0066268; Dame\Try1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 12 AA; 1301 MW; DF5820B9A84452D2 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RSW 4  
 DB 2 RSW 4

## RESULT 11

Q86CU1 ID Q86CU1 PRELIMINARY; PRT; 12 AA.  
 AC Q86CU1; 24, Created)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
 DE Trypsin 1 (Fragment)  
 GN Name=Try1; Synonyms=try1;  
 OS Drosophila novamexicana.  
 OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;  
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;  
 OC Ephydroidea; Drosophilidae; Drosophila.  
 OX NCBI\_TaxID=47314;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=15010-1031.0;  
 RX MEDLINE=22480340; PubMed=12574518; DOI=10.1073/pnas.0336368100;  
 RA Wittkopp P.J., Williams B.L., Selegue J.E., Carroll S.B.;  
 RT "Drosophila pigmentation evolution: divergent genotypes underlying  
 convergent phenotypes.";   
 RL Proc. Natl. Acad. Sci. U.S.A. 100:1808-1813 (2003).  
 DR EMBL; AY165534; AAP21578.1; -.  
 DR FlyBase; FBgn0066204; Dnov\Try1.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 12 AA; 1301 MW; DF5820B9A84452D2 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 12;  
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 RSW 4  
 DB 2 RSW 4

## Q9ZAM7

AC Q9ZAM7; 10, Created)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
 DE Endoglucanase (Fragment).  
 OS Cellvibrio japonicus.  
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Cellvibrion.  
 OX NCBI\_TaxID=155077;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cellulosa;  
 RX MEDLINE=90014181; PubMed=2507868;  
 RA Hall J., Hazlewood G.P., Huskisson N.S., Durrant A.J., Gilbert H.J.;  
 RT "Conserved serine-rich sequences in xylanase and cellulase from  
 Pseudomonas fluorescens subspecies cellulosa: internal sequence and  
 unusual protein processing.";   
 RL Mol. Microbiol. 31:1211-1219 (1989).  
 DR EMBL; X15429; CAA33470.1; -.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 12 AA; 1419 MW; 590020CF5AB69EB3 CRC64;

Query Match 27.0%; Score 20; DB 2; Length 12;  
 Best Local Similarity 75.0%; Pred. No. 1.3e+04;  
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 NRSC 12  
 DB 3 NRKC 6

## RESULT 12

Q70Y84 ID Q70Y84 PRELIMINARY; PRT; 8 AA.  
 AC Q70Y84; 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Ribosomal protein (Fragment).  
 GN Name=rp16;  
 OS Electranthus buchananii.  
 OC Chloroplast.  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;  
 OC Lamiales; Lamiaceae; Nepetoideae; Ocimeae; Plectranthus.  
 OX NCBI\_TaxID=204181;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC PubMed=15019625; DOI=10.1016/j.ympev.2003.08.002;  
 RA Paton A., Springate D.A., Sudde S., Otiemo D., Grayer R., Harley M.M.,  
 RA Willis F., Simmonds M.S.J., Powell M.P., Savolainen V.;  
 RT "Phylogeny and evolution of basil and allies (Ocimeae, Labiatae)  
 based on three plastid DNA regions.";   
 RL Mol. Phylogenet. Evol. 31:277-299 (2004).  
 DR EMBL; AJ505379; CAD45500.1; -.  
 DR GO; GO:0003735; F:Structural constituent of ribosome; IEA.  
 KW Ribosomal protein.  
 FT NON\_TER 1 1  
 SQ SEQUENCE 8 AA; 945 MW; 6EA415A5B5AB5863 CRC64;

Query Match 25.7%; Score 19; DB 2; Length 8;  
 Best Local Similarity 37.5%; Pred. No. 1.6e+06;  
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 WNKADNRS 11  
 DB 1 WGYCSSRS 8

## RESULT 13

Q7M124  
ID Q7M124 PRELIMINARY; PRT; 8 AA.  
AC Q7M124;  
DT 01-MAR-2004 (TrEMBLrel. 26, Created)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)  
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)  
DE Acylase.  
OS Kluyvera citrophila (Kluyvera cryocrescens).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;  
OC Enterobacteriaceae; Kluyvera.  
OX NCB1\_TaxID=580;  
RN [1]  
RP SEQUENCE.  
RA Martin J., Slade A., Aitken A., Arche R., Virden R.;  
RT "Chemical modification of serine at the active site of penicillin  
acylase from Kluyvera citrophila.";  
RL Biochem. J. 280:659-662(1991).  
DR PIR; S19288; S19288.  
SQ SEQUENCE 8 AA; 950 MW; CC387042D376944E CRC64;

Query Match 25.7%; Score 19; DB 2; Length 8;  
Best Local Similarity 50.0%; Pred. No. 1.6e+06;  
Matches 2; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSW 4  
Db 1 CNMW 4

## RESULT 14

Q6LBT3  
ID Q6LBT3 PRELIMINARY; PRT; 10 AA.  
AC Q6LBT3;  
DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
DE Ncam gene exon (pi) for neural cell adhesion molecule (NCAM).  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCB1\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Balb/c;  
RX MEDLINE=89251563; PubMed=2721486;  
RA Santoni M.J., Barthels D., Vopper G., Boned A., Goridis C., Wille W.;  
RT "Differential exon usage involving an unusual splicing mechanism  
generates at least eight types of NCAM cDNA in mouse brain.";  
RL ENBO J. 8:385-392(1989).  
DR EMBL; X14527; CAA32669.1;  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0016021; C:integral to membrane; TAS.  
SQ SEQUENCE 10 AA; 1231 MW; 3689D63B077411B3 CRC64;

Query Match 25.7%; Score 19; DB 2; Length 10;  
Best Local Similarity 25.0%; Pred. No. 1.5e+04;  
Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 SWNKADR 10  
Db 2 SWTRPEK 9

## RESULT 15

O77908  
ID O77908 PRELIMINARY; PRT; 11 AA.  
AC O77908;  
DT 01-NOV-1998 (TrEMBLrel. 08, Created)  
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)  
DE MHC class II B locus 2 (Fragment).  
OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidae;  
OC Cichlidae; Oreochromis.  
OX NCB1\_TaxID=8128;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=98315113; PubMed=9649539;  
RA Malaga-Trillo E., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,  
RA Figueroa F., Sultmann H., Klein J.;  
RT "Linkage relationships and haplotype polymorphism among cichlid MHC  
class II B loci.";  
RL Genetics 149:1527-1537(1998).  
DR EMBL; AF050019; AAC41358.1; -.  
FT NON TER 1 1  
SQ SEQUENCE 11 AA; 1261 MW; 4346CE9A7EB69EB3 CRC64;

Query Match 25.7%; Score 19; DB 2; Length 11;  
Best Local Similarity 40.0%; Pred. No. 1.7e+04;  
Matches 2; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 CRSW 5  
Db 5 CMCWS 9

Search completed: August 3, 2005, 12:38:36  
Job time : 168 secs

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GenCore version 5.1.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:20:34 ; Search time 158 Seconds  
(without alignments)  
29.374 Million cell updates/sec

Title: US-09-910-582B-10

Perfect score: 74

Sequence: 1 CRSWNKADNRSC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 520583

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A\_Geneseq\_16Dec04:\*  
1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	74	100.0	12	4	AAB30899 Peptide w
2	74	100.0	12	4	AAB59304 Heart hom
3	34	45.9	11	6	ABU59547 RGD bindi
4	33	44.6	12	2	AAR75854 Factor XI
5	32	43.2	11	6	ABU59550 RGD bindi
6	32	43.2	12	2	AA448838 Membrane
7	32	43.2	12	8	ADF78100 Factor VI
8	31	41.9	11	2	AAR34250 Mutant HT
9	31	41.9	12	2	AA448661 Membrane
10	31	41.9	12	8	ADF78103 Factor VI
11	30	40.5	10	2	AAR15780 Farnesyl-
12	30	40.5	10	2	AAR49741 Farnesyl-
13	30	40.5	10	2	AAR77803 Farnesyl-
14	30	40.5	10	2	AAW04433 Farnesyl
15	30	40.5	10	4	AAG96025 Human com
16	30	40.5	11	3	AAB10371 Geranylge
17	30	40.5	11	5	ABB98443 Lamine B
18	30	40.5	11	5	AAO22589 Carboxy t
19	30	40.5	11	5	ABB98445 Lamine B
20	30	40.5	11	5	ABB98447 Lamine B
21	30	40.5	12	8	ADF78096 Factor VI
22	29.5	39.9	11	5	ABP47645 N. mening
23	29.5	39.9	12	5	ABG60538 Selective
24	29	39.2	5	8	ADP06126 Cell adhe
25	29	39.2	6	8	ADP06145 Cell adhe

26	29	39.2	6	8	ADP06127 Cell adhe
27	29	39.2	7	8	ADP06128 Cell adhe
28	29	39.2	7	8	ADP06146 Cell adhe
29	29	39.2	8	8	ADP06129 Cell adhe
30	29	39.2	8	8	ADP06147 Cell adhe
31	29	39.2	8	8	ADP06148 Cell adhe
32	29	39.2	9	8	ADP06130 Cell adhe
33	29	39.2	10	4	AAG83522 Arabidops
34	29	39.2	10	8	ADP06131 Cell adhe
35	29	39.2	10	8	ADP06149 Cell adhe
36	29	39.2	11	6	ABU59549 RGD bindi
37	29	39.2	11	8	ADP06132 Cell adhe
38	29	39.2	11	8	ADP06130 Cell adhe
39	29	39.2	12	3	AA454523 Human CD4
40	29	39.2	12	7	ADL17593 Human MAG
41	29	39.2	12	8	ADK65054 PP1C-inte
42	29	39.2	12	8	ADP06151 Cell adhe
43	29	39.2	12	8	ADP06133 Cell adhe
44	28	37.8	9	2	AA410394 T cell ep
45	28	37.8	9	5	ABG80076 MHC class
46	28	37.8	9	8	ADK69015 Epitope 1
47	28	37.8	9	8	ADQ10813 Murine he
48	28	37.8	11	6	ABU59552 RGD bindi
49	28	37.8	12	2	AA448862 Membrane
50	27.5	37.2	9	5	ABP53959 VEGFR-3 b
51	27.5	37.2	9	5	ABJ04511 HUVEC cel
52	27	36.5	8	3	AB20992 Oligo-lys
53	27	36.5	9	3	AA494203 Human cyt
54	27	36.5	9	3	AA498763 Wtl deriv
55	27	36.5	9	3	AA498534 Wtl deriv
56	27	36.5	9	3	AA498652 Wtl deriv
57	27	36.5	9	3	AA498616 Wtl deriv
58	27	36.5	9	3	AA498743 Wtl deriv
59	27	36.5	9	3	AA498020 Human wtl
60	27	36.5	9	4	AA661948 Human wtl
61	27	36.5	9	4	AA661984 Human wtl
62	27	36.5	9	4	AA662095 Mouse wtl
63	27	36.5	9	4	AA661866 Human wtl
64	27	36.5	9	4	AA662075 Mouse wtl
65	27	36.5	9	4	AA668662 Mouse wtl
66	27	36.5	9	4	AA668633 Human wtl
67	27	36.5	9	4	AA668715 Human wtl
68	27	36.5	9	4	AA668751 Human wtl
69	27	36.5	9	4	AA668842 Mouse wtl
70	27	36.5	9	5	AB805262 Vascular
71	27	36.5	9	5	ABG33103 Human wtl
72	27	36.5	9	5	ABG33312 Mouse wtl
73	27	36.5	9	5	ABG33332 Mouse wtl
74	27	36.5	9	5	ABG33185 Human wtl
75	27	36.5	9	5	ABG33221 Human wtl
76	27	36.5	9	6	AB899881 Mouse wtl
77	27	36.5	9	6	ABR44359 Peptide #
78	27	36.5	9	6	ABR38975 Tumour su
79	27	36.5	9	6	ABR44450 Wtl origi
80	27	36.5	9	7	ADB67460 Mouse wtl
81	27	36.5	9	7	ADB67369 Human wtl
82	27	36.5	9	7	ADB67480 Mouse wtl
83	27	36.5	9	7	ADB67251 Human wtl
84	27	36.5	9	7	ADB67333 Human wtl
85	27	36.5	9	7	ADB677829 Synthetic
86	27	36.5	9	7	ADJ80484 Wilm's tu
87	27	36.5	9	7	ADJ80566 Wilm's tu
88	27	36.5	9	7	ADJ80602 Wilm's tu
89	27	36.5	9	7	ADJ80693 Wilm's tu
90	27	36.5	9	8	ADJ80713 Wilm's tu
91	27	36.5	9	8	ADJ80714 Human cox
92	27	36.5	9	8	ADJ83613 Murine wtl
93	27	36.5	9	8	ADJ83522 Human wtl
94	27	36.5	9	8	ADJ83633 Murine wtl
95	27	36.5	9	8	ADJ83404 Human wtl
96	27	36.5	9	8	ADJ83486 Human wtl
97	27	36.5	9	8	ADL57292 Human wtl
98	27	36.5	9	8	ADL57410 Human wtl

99 27 36.5 9 8 ADL57374 AdL57374 Human WT-  
100 27 36.5 9 8 ADL57521 AdL57521 Mouse WT-

## ALIGNMENTS

RESULT 1  
AAB30899  
ID AAB30899 standard; peptide; 12 AA.

AC AAB30899;  
XX 02-APR-2001 (first entry)  
XX Peptide which selectively binds to normal cardiac endothelium.  
XX Cardiac endothelium; angiogenic factor; vascular endothelium;  
KW peripheral vascular disease; cardiovascular disease; angiogenesis;  
KW cardiac neovascularisation.

XX Unidentified.

XX WO200075329-A1.  
PN 14-DEC-2000.

XX 31-MAY-2000; 2000WO-US014988.  
XX 07-JUN-1999; 99US-00327045.

XX (EDWA-) EDWARDS LIFESCIENCES CORP.  
PA (BAXT ) BAXTER AG.  
XX Levine AJ, Mitterer A, Falkner F, Scheiflinger F, Dorner F;  
PI WPI; 2001-091212/10.

XX New chimeric molecules having an angiogenic factor linked to a targeting  
PT molecule that binds to a vascular endothelium, useful for increasing  
PT cardiac neovascularization, or treating peripheral vascular and  
PT cardiovascular diseases.

XX Disclosure; Page 27; 67pp; English.

XX AAB30895-99 represent targeting molecules, which are used to produce the  
CC chimeric molecules of the invention. AAB30895-98 selectively bind to  
CC normal cardiac endothelium. The specification describes a chimeric  
CC molecule comprising an angiogenic factor linked to a targeting molecule  
CC that specifically binds to a vascular endothelium. The chimeric molecules  
CC are useful for treatment of peripheral vascular or cardiovascular  
CC diseases. Specifically, they are useful for inducing or inhibiting  
CC angiogenesis, for increasing cardiac neovascularisation in ischemic  
CC tissue in the peripheral vascular system

XX Sequence 12 AA;

Query Match 100.0%; Score 74; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12  
Db 1 CRSWNKADNRSC 12  
|||||

RESULT 2  
AAB59304  
ID AAB59304 standard; peptide; 12 AA.  
XX AAB59304;  
AC AAB59304;

XX 21-MAR-2001 (first entry)  
DT

XX Heart homing peptide SEQ ID NO: 10.  
DE  
XX Heart homing peptide; cardiovascular disease; ischaemic disease;  
KW gene therapy.  
XX Synthetic.

XX Key Location/Qualifiers  
FH Disulfide-bond 1..12  
FT /note= "disulfide bond cyclises the peptide"  
XX

XX WO200075174-A1.  
PN 14-DEC-2000.

XX 31-MAY-2000; 2000WO-US015088.  
XX 07-JUN-1999; 99US-00326718.

XX (BURN-) BURNHAM INST.  
XX Ruoslahti E, Mackenna DA;  
PI WPI; 2001-071059/08.

XX Novel heart homing peptide that selectively homes to normal ischemic and  
PT cardiac tissue useful for targeting ischemic tissues for treating  
PT ischemic and cardiovascular diseases such as atherosclerosis and  
PT restenosis.  
XX Claim 2; Page 55; 70pp; English.

XX The present invention provides a number of heart homing peptides which  
CC selectively home to cardiac tissue. These can be used in the treatment of  
CC cardiovascular and ischaemic diseases, such as atherosclerosis, myocardial  
CC thrombosis, restenosis, vasculitis, atherosclerotic aneurysms, myocardial  
CC hypertrophy, congenital heart diseases, ischaemic heart disease and  
CC anginas, acquired valvular/endocardial diseases, primary myocardial  
CC diseases, cardiac tumours and arrhythmias

XX Sequence 12 AA;

Query Match 100.0%; Score 74; DB 4; Length 12;  
Best Local Similarity 100.0%; Pred. No. 5.5e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12  
Db 1 CRSWNKADNRSC 12  
|||||

RESULT 3  
ABU59547  
ID ABU59547 standard; peptide; 11 AA.  
XX ABU59547;  
AC ABU59547;

XX 22-APR-2003 (first entry)  
DT  
XX RGD binding peptide #3.  
DE  
XX Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;  
KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;  
KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;  
KW tumour; cationic cancer-targeting peptide.

XX Synthetic.

XX US2002041898-A1.  
XX 11-APR-2002.  
PD  
XX

PF 25-JUL-2001; 2001US-00912609.  
 XX  
 PR 05-JAN-2000; 2000US-00478124.  
 PR 31-OCT-2000; 2000US-00703474.  
 XX  
 PA (UNGE//) UNGER E C.  
 PA (MATS//) MATSUNAGA T O.  
 PA (RAMA//) RAMASWAMI V.  
 PA (ROMA//) ROMANOWSKI M J.  
 XX  
 PI Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;  
 XX WPI; 2003-208921/20.  
 DR  
 XX Targeted delivery system comprising a bioactive agent homogeneously  
 XX dispersed in a targeted matrix is especially useful in cancer therapy.  
 PT  
 XX  
 PS Claim 44; Page 38; 46pp; English.  
 XX  
 CC The invention relates to a composition comprising a bioactive agent  
 CC homogeneously dispersed in a targeted matrix (polymer and targeting  
 CC ligand). Also included are a targeted matrix for use as a delivery  
 CC vehicle comprising a polymer associated with a targeting ligand,  
 CC enhancing the bioavailability of an agent comprising administration of  
 CC the composition and treating cancer comprising administration of the  
 CC novel composition. The method is useful for targeted delivery of a drug,  
 CC especially in cancer therapy. The targeting ligand may be a peptide.  
 CC Examples of targeting peptides are disclosed including cathepsin-D  
 CC substrate peptides, peptides targeting receptors in the brain and kidney,  
 CC peptides recognising fibronectin- and vitronectin-binding integrins,  
 CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,  
 CC peptides targeting the angiogenic endothelium of solid tumours, tissue  
 CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,  
 CC adrenal gland and retina), and cationic cancer-targeting peptides. The  
 CC present sequence is a peptide targeting ligand disclosed in the invention  
 XX  
 SQ Sequence 11 AA;  
 Query Match 45.9%; Score 34; DB 6; Length 11;  
 Best Local Similarity 60.0%; Pred. No. 1e+02;  
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;  
 QY 3 SWNKADNRSC 12  
 | : | | | | |  
 Db 2 SFKGQDNRIC 11  
 RESULT 4  
 AAR75854  
 ID AAR75854 standard; peptide; 12 AA.  
 XX  
 AC AAR75854;  
 XX  
 DT 11-MAR-1996 (first entry)  
 XX  
 DE Factor XI(a) platelet binding site peptide analogue.  
 XX  
 KW Factor XI(a); platelet binding site; peptide analogue; thrombosis;  
 KW antithrombotic agent; intrinsic coagulation.  
 XX  
 OS Synthetic.  
 XX  
 FH Key Location/Qualifiers  
 FT Disulfide-bond 1. .12  
 XX  
 PN W09517420-A1.  
 XX  
 PD 29-JUN-1995.  
 XX  
 XX 02-DEC-1994; 94WO-US013885.  
 PF  
 XX 22-DEC-1993; 93US-00172002.  
 PR  
 XX

PA (UTEM ) UNIV TEMPLE.  
 PA (UYJE-) UNIV JEFFERSON THOMAS.  
 XX  
 PI Walsh PN, Baglia PA, Jameson BA;  
 XX  
 DR WPI; 1995-240608/31.  
 XX  
 XX Peptide analogues of the factor XI platelet binding site - used to  
 PT specifically inhibit coagulation reactions involving factor XI and factor  
 PT XIa, for improved treatment of thrombosis.  
 PT  
 XX Claim 10; Page 79; 99pp; English.  
 PS  
 XX  
 CC AAR75854 is a factor XI(a) platelet binding site peptide analogue, useful  
 CC as an antithrombotic agent. The peptide specifically inhibits intrinsic  
 CC coagulation reactions, while leaving extrinsic reactions intact. This  
 CC permits normal hemostatic plug formation at a site of vascular injury,  
 CC minimising the risk of bleeding during antithrombotic therapy  
 XX  
 SQ Sequence 12 AA;  
 Query Match 44.6%; Score 33; DB 2; Length 12;  
 Best Local Similarity 41.7%; Pred. No. 1.6e+02;  
 Matches 5; Conservative 0; Mismatches 7; Indels 0; Gaps 0;  
 QY 1 CRSWNKADNRSC 12  
 | : | | | | |  
 Db 1 CPWPQESQRPC 12  
 RESULT 5  
 ABUS9550  
 ID ABUS9550 standard; peptide; 11 AA.  
 XX  
 AC ABUS9550;  
 XX  
 DT 22-APR-2003 (first entry)  
 XX  
 DE RGD binding peptide #6.  
 XX  
 KW Targeting ligand; bioactive agent; polymer matrix; cancer; cytostatic;  
 KW cathepsin-D substrate; peptides; neuroreceptor; adrenal receptor;  
 KW fibronectin; vitronectin; integrin; RGD motif; angiogenic endothelium;  
 KW tumour; cationic cancer-targeting peptide.  
 XX  
 OS Synthetic.  
 XX  
 PN US2002041898-A1.  
 XX  
 PD 11-APR-2002.  
 XX  
 PF 25-JUL-2001; 2001US-00912609.  
 XX  
 PR 05-JAN-2000; 2000US-00478124.  
 PR 31-OCT-2000; 2000US-00703474.  
 XX  
 XX (UNGE//) UNGER E C.  
 PA (MATS//) MATSUNAGA T O.  
 PA (RAMA//) RAMASWAMI V.  
 PA (ROMA//) ROMANOWSKI M J.  
 XX  
 XX Unger EC, Matsunaga TO, Ramaswami V, Romanowski MJ;  
 PI WPI; 2003-208921/20.  
 XX  
 XX Targeted delivery system comprising a bioactive agent homogeneously  
 PT dispersed in a targeted matrix is especially useful in cancer therapy.  
 PT  
 XX Claim 44; Page 38; 46pp; English.  
 PS  
 XX The invention relates to a composition comprising a bioactive agent  
 CC homogeneously dispersed in a targeted matrix (polymer and targeting  
 CC ligand). Also included are a targeted matrix for use as a delivery  
 CC vehicle comprising a polymer associated with a targeting ligand,  
 CC enhancing the bioavailability of an agent comprising administration of  
 CC the composition and treating cancer comprising administration of the  
 CC novel composition. The method is useful for targeted delivery of a drug,  
 CC especially in cancer therapy. The targeting ligand may be a peptide.  
 CC Examples of targeting peptides are disclosed including cathepsin-D  
 CC substrate peptides, peptides targeting receptors in the brain and kidney,  
 CC peptides recognising fibronectin- and vitronectin-binding integrins,  
 CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,  
 CC peptides targeting the angiogenic endothelium of solid tumours, tissue  
 CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,  
 CC adrenal gland and retina), and cationic cancer-targeting peptides. The  
 CC present sequence is a peptide targeting ligand disclosed in the invention  
 XX

CC vehicle comprising a polymer associated with a targeting ligand,  
 CC enhancing the bioavailability of an agent comprising administration of  
 CC the composition and treating cancer comprising administration of the  
 CC novel composition. The method is useful for targeted delivery of a drug,  
 CC especially in cancer therapy. The targeting ligand may be a peptide.  
 CC Examples of targeting peptides are disclosed including cathepsin-D  
 CC substrate peptides, peptides targeting receptors in the brain and kidney,  
 CC peptides recognising fibronectin- and vitronectin-binding integrins,  
 CC peptides targeting the RGD (Arg-Gly-Asp)-motif in, e.g., antibodies,  
 CC peptides targeting the angiogenic endothelium of solid tumours, tissue  
 CC specific peptides (e.g. of lung, skin, pancreas, intestine, uterus,  
 CC adrenal gland and retina), and cationic cancer- targeting peptides. The  
 CC present sequence is a peptide targeting ligand disclosed in the invention  
 XX

SQ Sequence 11 AA;

Query Match 43.2%; Score 32; DB 6; Length 11;  
 Best Local Similarity 50.0%; Pred. NO. 2.2e+02;  
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12  
 | : : : | : |  
 Db 2 SFGADRRNC 11

RESULT 6  
 AAY48838  
 ID AAY48838 standard; peptide; 12 AA.

AC AAY48838;

DT 20-MAR-2003 (revised)  
 DT 10-DEC-1999 (first entry)

XX Membrane dipeptidase-binding retina homing peptide #24.

XX Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;  
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;  
 KW membrane dipeptidase.

XX Synthetic.  
 OS Homo sapiens.

XX WO9946284-A2.

XX 16-SEP-1999.

XX 10-MAR-1999; 99WO-US005284.

XX 13-MAR-1998; 98US-00042107.

PR 26-FEB-1999; 99US-00258754.

XX (BURN-) BURNHAM INST.

XX Rajotte D, Pasqualini R, Ruoslahti ET;

XX WPI; 1999-571717/48.

XX New peptides which selectively home to organs or tissues, used for, e.g.  
 PT identifying target ligands and for therapy of pathological conditions.

XX Claim 28; Page 149; 193pp; English.

XX The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ or  
 CC tissue, for identifying a target molecule expressed by an organ or tissue  
 CC or for treating an organ or tissue pathology, where the organ or tissue  
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,  
 CC adrenal gland, liver, and lymph node. The peptide bind to the membrane  
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are  
 CC used in the exemplification of the present invention. (Updated on 20-MAR-  
 CC 2003 to correct PR field.)  
 XX

SQ Sequence 12 AA;

Query Match 43.2%; Score 32; DB 2; Length 12;  
 Best Local Similarity 41.7%; Pred. NO. 2.4e+02;  
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12  
 | : : : | : |  
 Db 1 CORVNSVENASC 12

RESULT 7

ADF78100  
 ID ADF78100 standard; peptide; 12 AA.

XX ADF78100;

XX 26-FEB-2004 (first entry)

XX Factor VIII peptidic mimic SEQ ID NO:13.

XX peptidic mimic; pseudopeptidic mimic; factor VIII; haemophilia A;  
 KW haemostatic; immunosuppressive; autoimmune disorder; haemorrhage.

XX Synthetic.

XX FR2830865-A1.

XX 18-APR-2003.

XX 17-OCT-2001; 2001FR-00013360.

XX 17-OCT-2001; 2001FR-00013360.

XX (CNRS ) CNRS CENT NAT RECH SCI.

XX Granier C, Villard S;

XX WPI; 2004-064179/07.

XX Peptide and pseudopeptide mimics of factor VIII that prevent disorders  
 PT due to the appearance of antibodies against factor VIII in hemophilic  
 PT patients.

XX Claim 10; SEQ ID NO 13; 36pp; French.

XX The invention relates to the novel use of peptidic and pseudopeptidic  
 CC mimics of factor VIII. The peptidic and pseudopeptidic mimics of factor  
 CC VIII are useful in medicines for the prevention and treatment of  
 CC disorders caused by the appearance of antibodies against endogenous or  
 CC exogenous factor VIII or its derivatives, which may be recombinant or  
 CC not, administered in cases of haemophilia A. A peptide of the invention  
 CC has haemostatic, and immunosuppressive activity. The compounds of the  
 CC invention are useful in the prevention and treatment of autoimmune  
 CC disorders and haemorrhage in patients with haemophilia A, especially  
 CC those that develop antibodies against factor VIII. The present sequence  
 CC is used in the exemplification of the invention.

SQ Sequence 12 AA;

Query Match 43.2%; Score 32; DB 8; Length 12;  
 Best Local Similarity 33.3%; Pred. NO. 2.4e+02;  
 Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12  
 | : : : | : |  
 Db 1 CSKWHNRSKRHC 12

RESULT 8

AAR34250  
 ID AAR34250 standard; peptide; 11 AA.

XX

AC AAR34250;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 04-AUG-1993 (first entry)  
 XX  
 DE Mutant HTLV-I residues 88-98, peptide 2L-1.4.  
 XX  
 KW Human T-cell leukaemia virus; hydrophilic; conjugate; aggregate;  
 KW diagnosis; antibodies; gp46; mutant; gag; T cell epitope.  
 XX  
 OS Synthetic.  
 XX  
 PN W09306843-A1.  
 XX  
 PD 15-APR-1993.  
 XX  
 PF 08-OCT-1992; 92WO-US008405.  
 XX  
 PR 08-OCT-1991; 91US-00771553.  
 XX  
 PA (UYDU-) UNIV DUKE.  
 XX  
 PI Palker TJ, Haynes BF;  
 XX  
 DR WPI; 1993-134125/16.  
 XX  
 XX Antigenic determinant peptide(s) of HTLV envelope glyco.protein - useful  
 PT for detecting anti-HTLV-I and -II antibodies and as vaccine against HTLV.  
 PT  
 XX Example 7; Page 32; 50pp; English.  
 XX  
 CC To determine which amino acids within the HTLV-I envelope amino acids 88-  
 CC 98 were required for absorption of neutralising anti-peptide antibodies  
 CC to HTLV-I, 11 peptides (2L1.1-2L1.11) were synthesised in which  
 CC sequential amino acids were each replaced by the amino acid alanine.  
 CC These 11 mutated peptides, as well as peptide 2L-1 bearing the native  
 CC HTLV-I sequence were tested and identified that amino acids 90, 92, 93  
 CC and 95 were important for HTLV-I neutralisation. See also AAR34225-57.  
 CC (Updated on 25-MAR-2003 to correct PN field.)  
 XX  
 SQ Sequence 11 AA;  
 Query Match 41.9%; Score 31; DB 2; Length 11;  
 Best Local Similarity 62.5%; Pred. No. 3.1e+02;  
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;  
 QY 4 WNKADNRS 11  
 DB 1 WTKAPNEN 8  
 |||||  
 |||||  
 RESULT 9  
 AAY48661  
 ID AAY48661 standard; peptide; 12 AA.  
 XX  
 AC AAY48661;  
 XX  
 DT 20-MAR-2003 (revised)  
 DT 10-DEC-1999 (first entry)  
 XX  
 DE Membrane dipeptidase-binding lung homing peptide #32.  
 XX  
 KW Homing peptide; organ; tissue; lung; pancreas; skin; retina; MDP;  
 KW prostate; ovary; lymph node; adrenal gland; liver; gut; tumour;  
 KW membrane dipeptidase.  
 XX  
 OS Synthetic.  
 OS Homo sapiens.  
 XX  
 PN W09946284-A2.  
 XX  
 PD 16-SEP-1999.  
 XX

PF 10-MAR-1999; 99WO-US005284.  
 XX  
 PR 13-MAR-1998; 98US-00042107.  
 PR 26-FEB-1999; 99US-00258754.  
 XX  
 PA (BURN-) BURNHAM INST.  
 XX  
 PI Rajotte D, Pasqualini R, Ruoslahti EI;  
 XX  
 DR WPI; 1999-571717/48.  
 XX  
 XX New peptides which selectively home to organs or tissues, used for, e.g.  
 PT identifying target ligands and for therapy of pathological conditions.  
 PT  
 XX Claim 11; Page 144; 193pp; English.  
 XX  
 CC The present invention describes peptides that selectively home to a  
 CC tissue or organ. The peptides can be used for identifying an organ or  
 CC tissue, for identifying a target molecule expressed by an organ or tissue  
 CC or for treating an organ or tissue pathology, where the organ or tissue  
 CC is selected from prostate, lung, skin, retina, pancreas, gut, ovary,  
 CC adrenal gland, liver and lymph node. The peptide bind to the membrane  
 CC dipeptidase (MDP). AAY48618 to AAY49066 represent sequences which are  
 CC used in the exemplification of the present invention. (Updated on 20-MAR-  
 CC 2003 to correct PR field.)  
 XX  
 SQ Sequence 12 AA;  
 Query Match 41.9%; Score 31; DB 2; Length 12;  
 Best Local Similarity 33.3%; Pred. No. 3.4e+02;  
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;  
 QY 1 CRSWNKADNRSC 12  
 DB 1 CRPWHNQAHTEC 12  
 |||||  
 |||||  
 RESULT 10  
 ADF78103  
 ID ADF78103 standard; peptide; 12 AA.  
 XX  
 AC ADF78103;  
 XX  
 DT 26-FEB-2004 (first entry)  
 XX  
 DE Factor VIII peptidic mimic SEQ ID NO:16.  
 XX  
 KW peptidic mimic; pseudopeptidic mimic; factor VIII; haemophilia A;  
 KW haemostatic; immunosuppressive; autoimmune disorder; haemorrhage..  
 XX  
 OS Synthetic.  
 XX  
 PN FR2830865-A1.  
 XX  
 PD 18-APR-2003.  
 XX  
 PF 17-OCT-2001; 2001FR-00013360.  
 XX  
 PR 17-OCT-2001; 2001FR-00013360.  
 XX  
 PA (CNRS ) CNRS CENT NAT RECH SCI.  
 XX  
 PI Granier C, Villard S;  
 XX  
 DR WPI; 2004-064179/07.  
 XX  
 PT Peptide and pseudopeptide mimics of factor VIII that prevent disorders  
 PT due to the appearance of antibodies against factor VIII in hemophilic  
 PT patients.  
 XX  
 PS Claim 10; SEQ ID NO 16; 36pp; French.  
 XX  
 CC The invention relates to the novel use of peptidic and pseudopeptidic

CC mimics of factor VIII. The peptidic and pseudopeptidic mimics of factor  
 CC VIII are useful in medicines for the prevention and treatment of  
 CC disorders caused by the appearance of antibodies against endogenous or  
 CC exogenous factor VIII or its derivatives, which may be recombinant or  
 CC not, administered in cases of haemophilia A. A peptide of the invention  
 CC has haemostatic, and immunosuppressive activity. The compounds of the  
 CC invention are useful in the prevention and treatment of autoimmune  
 CC disorders and haemorrhage in patients with haemophilia A, especially  
 CC those that develop antibodies against factor VIII. The present sequence  
 CC is used in the exemplification of the invention.

XX  
 SQ Sequence 12 AA;

Query Match 41.9%; Score 31; DB 8; Length 12;  
 Best Local Similarity 33.3%; Pred. No. 3.4e+02;  
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 CRSWNKADNRSC 12  
 | | : | |  
 Db 1 CMKWSNRSSRWC 12

RESULT 11  
 AAR15780  
 ID AAR15780 standard; protein; 10 AA.

AC AAR15780;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 09-JAN-2003 (revised)  
 DT 29-JAN-1992 (first entry)  
 XX  
 DE Farnesyl-protein transferase inhibitor (33).  
 XX  
 KW Farnesyl; transferase; FT; inhibitor; p21ras; rat.  
 XX  
 OS Synthetic.

Key Location/Qualifiers  
 FT Peptide 7. 10

XX WO9116340-A.  
 XX 31-OCT-1991.  
 XX 18-APR-1990; 90US-00510706.  
 XX 18-APR-1990; 90US-00510706.  
 XX 20-NOV-1990; 90US-00615715.  
 XX (TEXA ) UNIV TEXAS SYSTEM.

XX Brown MS, Goldstein JL, Reiss Y;  
 PI WPI; 1991-339750/46.

XX Compn. comprising purified farnesyl-protein transferase - used to  
 PT inhibit attachment of farnesyl moiety to RAS protein in malignant cells  
 PT and to treat cancer.

XX Claim 25; Page 68; 87pp; English.

XX This peptide, the fragment indicated in the features, or the peptides  
 CC represented in AAR15751-81, AAR14723 and AAR14711 inhibit the rat FTS  
 CC represented in AAR14712-22. They show FT inhibition at an IC50 of 0.01-10  
 CC microm. The most potent inhibitors are ones in which phenylalanine occurs  
 CC at the third position of a tetrapeptide whose N-terminus is cysteine. The  
 CC inhibitors have a farnesyl acceptor or inhibitor sequence within its  
 CC structure and are capable of inhibiting the farnesylation of p21ras by  
 CC FT. See also AAR14711-23 and AAQ14541-47. (Updated on 09-JAN-2003 to add  
 CC missing OS field.) (Updated on 25-MAR-2003 to correct PA field.)

XX Sequence 10 AA;

Query Match 40.5%; Score 30; DB 2; Length 10;  
 Best Local Similarity 71.4%; Pred. No. 4e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KADNRSC 12  
 : | | | |  
 Db 1 RASNRSC 7

RESULT 12  
 AAR49741  
 ID AAR49741 standard; peptide; 10 AA.

XX  
 AC AAR49741;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 08-AUG-1994 (first entry)  
 XX  
 DE Farnesyltransferase-inhibitor.

XX Farnesyltransferase-inhibitor; farnesyltransferase; FT; p21ras;  
 KW ras protein; farnesylation; cancer therapy.  
 XX  
 OS Synthetic.

XX WO9404561-A1.  
 XX 03-MAR-1994.  
 XX 24-AUG-1993; 93WO-US008062.  
 XX 24-AUG-1992; 92US-00935087.

XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA (GETH ) GENENTECH INC.

XX Brown MS, Goldstein JL, Reiss Y, Marsters JC;  
 PI WPI; 1994-083105/10.

XX New farnesyl-transferase inhibitors - used for inhibiting attachment of a  
 PT farnesyl moiety to a p21ras protein in malignant cells.  
 XX Disclosure; Page 33; 183pp; English.

XX Peptides given in AAR49741-75, AAR49777-78 and AAR49785-88, which include  
 CC a family of tetrapeptides based on the recognition site (AAR49776) of  
 CC farnesyltransferase (FT), are potential anticancer agents that inhibit  
 CC FT, thereby preventing expression of p21ras. (Updated on 25-MAR-2003 to  
 CC correct PN field.)

XX Sequence 10 AA;

Query Match 40.5%; Score 30; DB 2; Length 10;  
 Best Local Similarity 71.4%; Pred. No. 4e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 KADNRSC 12  
 : | | | |  
 Db 1 RASNRSC 7

RESULT 13  
 AAR77803  
 ID AAR77803 standard; protein; 10 AA.

XX AAR77803;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 23-JAN-1996 (first entry)  
 XX  
 DE Farnesyl transferase inhibitor peptide, RASNRSCAIM.

XX Farnesyl transferase; inhibitor; cancer; ras; p21.  
 XX Synthetic.  
 OS US5420245-A.  
 PN 30-MAY-1995.  
 PD 03-APR-1992; 92US-00863169.  
 PF 18-APR-1990; 90US-00510706;  
 XX 20-NOV-1990; 90US-00615715.  
 PR 16-JAN-1992; 92US-00822011.  
 XX (TEXA ) UNIV TEXAS.  
 PA Reiss Y, Goldstein JL, Brown MS;  
 PI WPI; 1995-206308/27.  
 XX New farnesyl transferase inhibitor peptide(s) - based on farnesyl  
 PT acceptor substrate carboxy terminal sequences, used for the treatment of  
 PT cancer.  
 XX Claim 2; Col 61; 55pp; English.  
 PS AAR77801-R77804 are peptide inhibitors of farnesyl transferase. They all  
 XX have a C-terminal sequence obeying the generic formula -CAXX,  
 CC where C= cysteine, A= any aliphatic, aromatic or hydroxy amino acid and  
 CC X= any normal amino acid. Farnesyl transferase is involved in the  
 CC farnesylation of various cellular proteins including the cancer related  
 CC ras proteins. The transforming activity of ras is dependent on the  
 CC localisation of the protein to membranes, a property which is thought to  
 CC be dependent upon the addition of farnesyl groups. The peptide inhibitors  
 CC are useful for treating cancers and ras-related cancers in particular.  
 CC (Updated on 25-MAR-2003 to correct PF field.)  
 XX SQ Sequence 10 AA;  
 Query Match 40.5%; Score 30; DB 2; Length 10;  
 Best Local Similarity 71.4%; Pred. No. 4e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 KADNRSC 12  
 DB :| |||||  
 1 RASNRSC 7  
 RESULT 14  
 ID AAW04433 standard; peptide; 10 AA.  
 AC AAW04433;  
 XX 30-JUL-1997 (first entry)  
 DT Farnesyl transferase peptide inhibitor used in cancer treatment.  
 XX Farnesyl transferase; inhibitor; cancer; tumour; neoplasia; prenyl;  
 KW ras protein; K-ras B; malignant; detection; identification.  
 XX Synthetic.  
 OS WO9634113-A2.  
 PN 31-OCT-1996.  
 PD 29-APR-1996; 96WO-US005969.  
 PF 27-APR-1995; 95US-00429964.  
 XX (TEXA ) UNIV TEXAS SYSTEM.  
 PA

XX Brown MS, Goldstein JL, James GL;  
 PI WPI; 1996-497642/49.  
 DR Assay for farnesyl transferase activity - by determining ability to  
 XX transfer farnesyl moiety to K-Ras B protein, partic. useful for  
 PT identifying inhibitors.  
 PT Disclosure; Page 33; 257pp; English.  
 PS AAW04433-W04465 are peptide inhibitors of farnesyl transferase (FT)  
 XX activity. The peptides block the attachment of prenyl groups to ras  
 CC proteins in malignant cells of patients suffering from cancer or a  
 CC precancerous state and as such are used to treat cancer. The peptides  
 CC were identified by determining the ability of candidate substances to  
 CC inhibit a FT enzyme, by inhibiting the transfer of a farnesyl moiety to a  
 CC K-RasB protein  
 XX SQ Sequence 10 AA;  
 Query Match 40.5%; Score 30; DB 2; Length 10;  
 Best Local Similarity 71.4%; Pred. No. 4e+02;  
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
 QY 6 KADNRSC 12  
 DB :| |||||  
 1 RASNRSC 7  
 RESULT 15  
 ID AAG96025 standard; peptide; 10 AA.  
 XX AAG96025;  
 AC AAG96025;  
 XX 18-SEP-2001 (first entry)  
 DT Human complementary peptide, SEQ ID NO: 2219.  
 XX Human; complementary peptide; ligand; drug discovery; drug design.  
 KW Homo sapiens.  
 OS WO200142277-A2.  
 XX 14-JUN-2001.  
 PD 13-DEC-2000; 2000WO-GB004776.  
 PF 13-DEC-1999; 99GB-00029464.  
 PR (PROT-) PROTEOM LTD.  
 XX Roberts GW, Heal JR;  
 XX WPI; 2001-408419/43.  
 DR A set of peptide ligands consisting of specific complementary peptides to  
 XX proteins encoded by genes of the human genome, useful in an assay for  
 PT screening and identifying of one or more novel peptides which are drug  
 PT candidates or pro-drugs.  
 XX Example 4; Page 360; 646pp; English.  
 PS The invention relates to a set of complementary peptide ligands generated  
 XX from the human genome. The complementary peptides interact with their  
 CC relevant target proteins encoded in the human genome. They can be used as  
 CC reagents in drug discovery and as lead ligands to facilitate drug design  
 CC and development. The present sequence is a complementary peptide provided  
 CC in the specification  
 XX SQ Sequence 10 AA;

Query Match 40.5%; Score 30; DB 4; Length 10;  
Best Local Similarity 44.4%; Pred. No. 4e+02;  
Matches 4; Conservative 1; Mismatches 0; Gaps 0;  
Indels 4;

Qy 1 CRSWNKADN 9  
| : | | |  
Db 1 CORWEKLQN 9

Search completed: August 3, 2005, 12:35:45  
Job time : 161 secs



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OM protein - protein search, using sw model

Run on: August 3, 2005, 12:30:30 ; Search time 41 Seconds  
(without alignments)  
21.849 Million cell updates/sec

Title: US-09-910-582B-10

Perfect score: 74

Sequence: 1 CROWNKADNRSC 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 135920

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Issued Patents AA:\*  
1: /cgn2\_6/ptodata/1/iaa/5A COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCPUS COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	100.0	12	3	US-09-326-718-10
2	32	43.2	12	3	US-09-258-754-244
3	32	43.2	12	3	US-09-042-107-244
4	32	43.2	12	4	US-09-722-250D-244
5	32	43.2	12	4	US-09-676-475A-244
6	31	41.9	11	1	US-08-116-733-34
7	31	41.9	12	3	US-09-258-754-82
8	31	41.9	12	3	US-09-042-107-82
9	31	41.9	12	4	US-09-722-250D-82
10	31	41.9	12	4	US-09-676-475A-82
11	30	40.5	10	2	US-08-429-964-15
12	30	40.5	10	5	PCT-US93-08062-15
13	29	39.2	12	3	US-09-100-409A-24
14	28	37.8	11	5	PCT-US94-01234-71
15	28	37.8	12	3	US-09-258-754-263
16	28	37.8	12	3	US-09-042-107-263
17	28	37.8	12	4	US-09-722-250D-263
18	28	37.8	12	4	US-09-676-475A-263
19	27	36.5	11	8	US-08-990-015-11
20	27	36.5	11	5	PCT-US94-01234-69
21	26	35.1	6	1	US-08-375-911A-4
22	26	35.1	7	4	US-09-036-461-1
23	26	35.1	11	1	US-08-116-733-1
24	26	35.1	11	1	US-08-116-733-38
25	26	35.1	11	1	US-08-116-733-39
26	26	35.1	11	1	US-08-116-733-40
27	26	35.1	11	1	US-08-116-733-41

28	35.1	12	3	US-09-258-754-232	Sequence 232, App
29	35.1	12	3	US-09-042-107-232	Sequence 232, App
30	35.1	12	4	US-09-722-250D-232	Sequence 232, App
31	35.1	12	4	US-09-676-475A-232	Sequence 232, App
32	35.1	12	3	US-09-258-754-64	Sequence 64, Appl
33	35.1	12	3	US-09-042-107-64	Sequence 64, Appl
34	35.1	9	4	US-09-722-250D-64	Sequence 64, Appl
35	35.1	9	4	US-09-676-475A-64	Sequence 64, Appl
36	35.1	7	1	US-08-460-343B-6	Sequence 6, Appl
37	35.1	7	1	US-08-398-028B-6	Sequence 6, Appl
38	35.1	7	2	US-08-504-265B-6	Sequence 6, Appl
39	35.1	8	5	PCT-US95-11127-15	Sequence 15, Appl
40	35.1	8	5	US-09-258-754-378	Sequence 378, App
41	35.1	9	3	US-09-042-107-378	Sequence 378, App
42	35.1	9	4	US-09-722-250D-378	Sequence 378, App
43	35.1	9	4	US-09-676-475A-378	Sequence 378, App
44	35.1	10	3	US-08-925-002-9	Sequence 9, Appl
45	35.1	10	3	US-08-893-526A-14	Sequence 14, Appl
46	35.1	10	3	US-08-630-915A-46	Sequence 46, Appl
47	35.1	10	4	US-09-910-552-9	Sequence 9, Appl
48	35.1	10	4	US-09-879-957-46	Sequence 46, Appl
49	35.1	11	1	US-08-116-733-35	Sequence 35, Appl
50	35.1	11	5	PCT-US94-01234-12	Sequence 12, Appl
51	35.1	12	1	US-07-778-233B-44	Sequence 44, Appl
52	35.1	12	1	US-07-963-321-44	Sequence 44, Appl
53	35.1	12	1	US-08-290-641-44	Sequence 44, Appl
54	35.1	12	1	US-08-548-540-44	Sequence 44, Appl
55	35.1	12	5	PCT-US96-09809-44	Sequence 44, Appl
56	35.1	10	1	US-08-077-797A-7	Sequence 7, Appl
57	35.1	10	4	US-09-546-013-36	Sequence 36, Appl
58	35.1	10	5	PCT-US94-01238-7	Sequence 7, Appl
59	35.1	11	4	US-09-069-827A-40	Sequence 40, Appl
60	35.1	5	3	US-09-270-957-32	Sequence 32, Appl
61	35.1	6	3	US-09-258-754-173	Sequence 173, App
62	35.1	6	3	US-09-042-107-173	Sequence 173, App
63	35.1	6	4	US-09-722-250D-173	Sequence 173, App
64	35.1	6	4	US-09-676-475A-173	Sequence 173, App
65	35.1	7	1	US-08-253-854-68	Sequence 68, Appl
66	35.1	7	4	US-09-535-852-952	Sequence 952, App
67	35.1	7	4	US-09-535-852-1008	Sequence 1008, App
68	35.1	8	1	US-08-526-710-7	Sequence 7, Appl
69	35.1	8	3	US-08-862-855-7	Sequence 7, Appl
70	35.1	8	3	US-09-226-985-7	Sequence 7, Appl
71	35.1	8	3	US-09-227-906-7	Sequence 7, Appl
72	35.1	8	4	US-09-535-852-959	Sequence 959, App
73	35.1	8	4	US-09-535-852-1015	Sequence 1015, App
74	35.1	8	4	US-09-535-852-1233	Sequence 1233, App
75	35.1	8	4	US-09-535-852-1281	Sequence 1281, App
76	35.1	8	4	US-09-328-866-7	Sequence 7, Appl
77	35.1	9	1	US-08-526-710-13	Sequence 13, Appl
78	35.1	9	3	US-08-862-855-13	Sequence 13, Appl
79	35.1	9	3	US-09-258-754-328	Sequence 328, App
80	35.1	9	3	US-09-042-107-328	Sequence 328, App
81	35.1	9	3	US-09-226-985-13	Sequence 13, Appl
82	35.1	9	3	US-09-227-906-13	Sequence 13, Appl
83	35.1	9	4	US-09-722-250D-328	Sequence 328, App
84	35.1	9	4	US-09-535-852-1038	Sequence 1038, App
85	35.1	9	4	US-09-535-852-1039	Sequence 1039, App
86	35.1	9	4	US-09-535-852-1240	Sequence 1240, App
87	35.1	9	4	US-09-535-852-1288	Sequence 1288, App
88	35.1	9	4	US-09-328-866-13	Sequence 13, Appl
89	35.1	9	4	US-09-676-475A-328	Sequence 328, App
90	35.1	10	4	US-09-535-852-1045	Sequence 1045, App
91	35.1	10	4	US-09-535-852-1046	Sequence 1046, App
92	35.1	11	1	US-08-116-733-32	Sequence 32, Appl
93	35.1	12	2	US-08-764-640-84	Sequence 84, Appl
94	35.1	12	3	US-08-973-225-84	Sequence 84, Appl
95	35.1	12	3	US-09-244-298A-84	Sequence 84, Appl
96	35.1	12	3	US-09-258-754-236	Sequence 236, App
97	35.1	12	3	US-09-042-107-236	Sequence 236, App
98	35.1	12	3	US-09-516-704-84	Sequence 84, Appl
99	35.1	12	3	US-09-025-769B-184	Sequence 184, App
100	35.1	12	4	US-09-549-090-84	Sequence 84, Appl

## ALIGNMENTS

RESULT 1  
US-09-326-718-10  
; Sequence 10, Application US/09326718  
; Patent No. 6303573  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Mackenna, Deirdre A.  
; TITLE OF INVENTION: Heart Homing Peptides and Methods of  
; TITLE OF INVENTION: Using Same  
; FILE REFERENCE: P-LJ 3512  
; CURRENT APPLICATION NUMBER: US/09/326,718  
; CURRENT FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-326-718-10

Query Match 100.0%; Score 74; DB 3; Length 12;  
Best Local Similarity 100.0%; Pred. No. 3.3e-05;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12  
Db 1 CRSWNKADNRSC 12  
|||||

RESULT 2  
US-09-258-754-244  
; Sequence 244, Application US/09258754  
; Patent No. 6174687  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Dipeptidase  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 244  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-244

Query Match 43.2%; Score 32; DB 3; Length 12;  
Best Local Similarity 41.7%; Pred. No. 82;  
Matches 5; Conservative 2; Mismatches 5; Indels 5; Gaps 0;

Qy 1 CRSWNKADNRSC 12  
Db 1 CORVNSVENASC 12  
|:|:|

RESULT 3  
US-09-042-107-244  
; Sequence 244, Application US/09042107

; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 244  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-244

Query Match 43.2%; Score 32; DB 3; Length 12;  
Best Local Similarity 41.7%; Pred. No. 82;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12  
Db 1 CORVNSVENASC 12  
|:|:|

RESULT 4  
US-09-722-250D-244  
; Sequence 244, Application US/09722250D  
; Patent No. 6610651  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 4514  
; CURRENT APPLICATION NUMBER: US/09/722,250D  
; CURRENT FILING DATE: 2000-11-22  
; PRIOR APPLICATION NUMBER: US 09/042,107  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 437  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 244  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-722-250D-244

Query Match 43.2%; Score 32; DB 4; Length 12;  
Best Local Similarity 41.7%; Pred. No. 82;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12  
Db 1 CORVNSVENASC 12  
|:|:|

RESULT 5  
US-09-676-475A-244  
; Sequence 244, Application US/09676475A  
; Patent No. 6784153  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Dipeptidase  
; FILE REFERENCE: P-LA 4377  
; CURRENT APPLICATION NUMBER: US/09/676,475A

; CURRENT FILING DATE: 1998-03-13  
; PRIOR APPLICATION NUMBER: 09/042,107  
; PRIOR FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 244  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-676-475A-244

Query Match 43.2%; Score 32; DB 4; Length 12;  
Best Local Similarity 41.7%; Pred. No. 82;  
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12  
Db 1 CORVNSVENASC 12

RESULT 6  
US-08-116-733-34  
; Sequence 34, Application US/08116733  
; Patent No. 5516632  
; GENERAL INFORMATION:  
; APPLICANT: PALKER, Thomas J.  
; APPLICANT: HAYNES, Barton F.  
; TITLE OF INVENTION: SYNTHETIC PEPTIDES  
; NUMBER OF SEQUENCES: 46  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: NIXON & VANDERHVE P.C.  
; STREET: 1100 NORTH GLEBE ROAD  
; CITY: ARLINGTON  
; STATE: VIRGINIA  
; COUNTRY: U.S.A.  
; ZIP: 22201-4714  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/116,733  
; FILING DATE: 07-SEP-1993  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: WILSON, MARY J.  
; REGISTRATION NUMBER: 32,955  
; REFERENCE/DOCKET NUMBER: 1579-33  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (703) 816-4000  
; TELEFAX: (703) 816-4100  
; TELEX: 200797 NIXN UR  
; INFORMATION FOR SEQ ID NO: 34:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
US-08-116-733-34

Query Match 41.9%; Score 31; DB 1; Length 11;  
Best Local Similarity 62.5%; Pred. No. 1.1e+02;  
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 WNKADNES 11  
Db 1 WTKAPNRN 8

RESULT 7

US-09-258-754-82  
; Sequence 82, Application US/09258754  
; Patent No. 6174687  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; TITLE OF INVENTION: Membrane Dipeptidase  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107  
; EARLIER FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 452  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-258-754-82

Query Match 41.9%; Score 31; DB 3; Length 12;  
Best Local Similarity 33.3%; Pred. No. 1.2e+02;  
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12  
Db 1 CRPWHNQAHTEC 12

RESULT 8  
US-09-042-107-82  
; Sequence 82, Application US/09042107  
; Patent No. 6232287  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues  
; FILE REFERENCE: P-LJ 2892  
; CURRENT APPLICATION NUMBER: US/09/042,107  
; CURRENT FILING DATE: 1998-03-13  
; NUMBER OF SEQ ID NOS: 436  
; SOFTWARE: PatentIn Ver. 2.0  
; SEQ ID NO 82  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
US-09-042-107-82

Query Match 41.9%; Score 31; DB 3; Length 12;  
Best Local Similarity 33.3%; Pred. No. 1.2e+02;  
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12  
Db 1 CRPWHNQAHTEC 12

RESULT 9  
US-09-722-250D-82  
; Sequence 82, Application US/09722250D  
; Patent No. 6610651  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or  
; TITLE OF INVENTION: Tissues

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; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/09/722,250D
; CURRENT FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-722-250D-82

Query Match 41.9%; Score 31; DB 4; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
Db 1 CRPWHQAHTEC 12

RESULT 10
US-09-676-475A-82
; Sequence 82, Application US/09676475A
; Patent No. 6784153
; GENERAL INFORMATION:
; APPLICANT: Ruolahti, Erkki
; APPLICANT: Pasqualini, Renata
; APPLICANT: Rajotte, Daniel
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using
; TITLE OF INVENTION: Membrane Dipeptidase
; FILE REFERENCE: P-LA 4377
; CURRENT APPLICATION NUMBER: US/09/676,475A
; CURRENT FILING DATE: 1998-03-13
; PRIOR APPLICATION NUMBER: 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-676-475A-82

Query Match 41.9%; Score 31; DB 4; Length 12;
Best Local Similarity 33.3%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 CRSWNKADNRSC 12
Db 1 CRPWHQAHTEC 12

RESULT 11
US-08-429-964-15
; Sequence 15, Application US/08429964
; Patent No. 5962243
; GENERAL INFORMATION:
; APPLICANT: BROWN, MICHAEL S.
; APPLICANT: GOLDSTEIN, JOSEPH L.
; APPLICANT: REISS, YUVAL
; APPLICANT: JAMES, GUY L.
; TITLE OF INVENTION: METHODS FOR THE IDENTIFICATION OF FARNESYL
; TITLE OF INVENTION: TRANSFERASE INHIBITORS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433

```

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; CITY: HOUSTON
; STATE: TEXAS
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,964
; FILING DATE: 27-APR-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/021,625
; FILING DATE: 16-FEB-1993
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/822,011
; FILING DATE: ABANDONED
; CLASSIFICATION: 435
; APPLICATION NUMBER: PCT/US/91/02650
; FILING DATE: 18-APR-1991
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/615,715
; FILING DATE: 20-NOV-1990
; CLASSIFICATION: 435
; APPLICATION NUMBER: US 07/510,706
; FILING DATE: 18-APR-1990 (ABANDONED)
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: PARKER, DAVID L.
; REGISTRATION NUMBER: 32,165
; REFERENCE/DOCKET NUMBER: UTSD:432/PAR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (512) 418-3000
; TELEFAX: (713) 789-2679
; TELEX: 79-0924
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 10 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-429-964-15

Query Match 40.5%; Score 30; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 KADNRSC 12
Db 1 RASNRSC 7

RESULT 12
PCT-US93-08062-15
; Sequence 15, Application PC/TUS9308062
; GENERAL INFORMATION:
; APPLICANT:
; SEQUENCE CHARACTERISTICS:
; SEQUENCE CHARACTERISTICS: BROWN, MICHAEL S.
; SEQUENCE CHARACTERISTICS: GOLDSTEIN, JOSEPH L.
; SEQUENCE CHARACTERISTICS: REISS, YUVAL
; SEQUENCE CHARACTERISTICS: MARSTERS, JR., JAMES C.
; ADDRESSEE: METHODS AND COMPOSITIONS FOR
; ADDRESSEE: THE IDENTIFICATION
; ADDRESSEE: CHARACTERIZATION AND
; ADDRESSEE: INHIBITION OF
; ADDRESSEE: FARNESYLTRANSFERASE
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ARNOLD, WHITE & DURKEE
; STREET: P.O. BOX 4433

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;  
; CITY: HOUSTON  
; STATE: TEXAS  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 77210  
; MEDIUM TYPE: FLOPPY DISK/ASKII  
; COMPUTER: IBM PC COMPATIBLE  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: WORDPERFECT 5.1  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US93/08062  
; FILING DATE: AUGUST 24, 1993  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/935,087  
; FILING DATE: 24 AUGUST 1992 (24.08.92)  
; NAME: UNKNOWN  
; ATTORNEY/AGENT INFORMATION:  
; NAME: PARKER, DAVID L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTFD377PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512-320-7200  
; TELEFAX: 512-474-7577  
; TELEX: NOT APPLICABLE  
; INFORMATION FOR SEQ ID NO: 15:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 10 amino acid residues  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; PCT-US93-08062-15  
  
Query Match 40.5%; Score 30; DB 5; Length 10;  
Best Local Similarity 71.4%; Pred. No. 1.4e+02;  
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;  
  
QY 6 KADNRSC 12  
Db 1 RASNRSC 7  
  
RESULT 13  
US-09-100-409A-24  
; Sequence 24, Application US/09100409A  
; Patent No. 6090388  
; GENERAL INFORMATION:  
; APPLICANT: Wang, Chang Yi  
; TITLE OF INVENTION: PEPTIDE COMPOSITION FOR  
; PREVENTION AND TREATMENT OF HIV INFECTION AND  
; IMMUNE DISORDERS  
; NUMBER OF SEQUENCES: 64  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MORGAN & FINNEGAN  
; STREET: 345 Park Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10154-0054  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version  
; SOFTWARE: #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/100,409A  
; FILING DATE:  
; CLASSIFICATION: 514  
; ATTORNEY/AGENT INFORMATION:  
; NAME:  
; REGISTRATION NUMBER:  
; REFERENCE/DOCKET NUMBER: 1151-4154

;  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212-758-4800  
; TELEFAX: 212-751-6849  
; INFORMATION FOR SEQ ID NO: 24:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 12 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-09-100-409A-24  
  
Query Match 39.2%; Score 29; DB 3; Length 12;  
Best Local Similarity 33.3%; Pred. No. 2.4e+02;  
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;  
  
QY 1 CRSMNKADNRSC 12  
Db 1 CKGPSKLNDRAC 12  
  
RESULT 14  
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; Sequence 71, Application PC/TUS9401234  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE  
; BINDING SITES  
; NUMBER OF SEQUENCES: 76  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US94/01234  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/084,542  
; FILING DATE: 28-JUN-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US'08/012,566  
; FILING DATE: 02-FEB-1993  
; INFORMATION FOR SEQ ID NO: 71:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 11 amino acids  
; TYPE: amino acid  
; TOPOLOGY: both  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
; PCT-US94-01234-71  
  
Query Match 37.8%; Score 28; DB 5; Length 11;  
Best Local Similarity 40.0%; Pred. No. 3.1e+02;  
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;  
  
QY 3 SMNKADNRSC 12  
Db 2 SPQRTDQRNC 11  
  
RESULT 15  
US-09-258-754-263  
; Sequence 263, Application US/09258754  
; Patent No. 6174687  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Pasqualini, Renata  
; APPLICANT: Rajotte, Daniel  
; TITLE OF INVENTION: Methods of Identifying Lung Homing Molecules Using  
; DIPEPTIDASE  
; FILE REFERENCE: P-LJ 3443  
; CURRENT APPLICATION NUMBER: US/09/258,754  
; CURRENT FILING DATE: 1999-02-26  
; EARLIER APPLICATION NUMBER: 09/042,107

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; EARLIER FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 452
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 283
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-258-754-263
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Query Match      37.8%; Score 28; DB 3; Length 12;
Best Local Similarity 41.7%; Pred. No. 3.3e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 CRSWNKADNRSC 12
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Db      1 CRARIRAEIDISC 12
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Job time : 42 secs
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 12:38:46 ; Search time 152 Seconds  
(without alignments)  
30.759 Million cell updates/sec

Title: US-09-910-582B-10

Perfect score: 74

Sequence: 1 CRSWNKADNRSC 12

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Gapop 10.0 , Gapext 0.5

Searched: 1745140 seqs, 389608008 residues

Total number of hits satisfying chosen parameters: 243143

Minimum DB seq length: 0

Maximum DB seq length: 12

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

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3: /cgn2\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*  
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11: /cgn2\_6/ptodata/2/pubpaa/US09C\_PUBCOMB.pep.\*  
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21: /cgn2\_6/ptodata/2/pubpaa/US60\_NEW\_PUB.pep.\*  
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	74	100.0	12	10	US-09-910-582B-10
3	74	100.0	12	17	US-10-838-289-38
4	34	45.9	11	9	US-09-912-609-22
5	34	45.9	11	17	US-10-838-289-78
6	32	43.2	11	9	US-09-912-609-25
7	32	43.2	11	17	US-10-838-289-81
8	32	43.2	12	17	US-10-838-289-301
9	32	43.2	12	17	US-10-607-595-244
10	32	43.2	12	18	US-10-492-929-13
11	31	41.9	12	17	US-10-838-289-189

31	41.9	12	17	US-10-607-595-82	Sequence 82, Appl
31	41.9	12	18	US-10-492-929-16	Sequence 16, Appl
30	40.5	10	10	US-09-572-404B-2219	Sequence 2219, Ap
30	40.5	12	18	US-10-492-929-9	Sequence 9, Appli
29.5	39.9	11	15	US-10-398-104-221	Sequence 221, App
29.5	39.9	12	16	US-10-363-204-219	Sequence 219, App
29	39.2	5	16	US-10-714-564A-303	Sequence 303, App
29	39.2	6	16	US-10-714-564A-304	Sequence 304, App
29	39.2	6	16	US-10-714-564A-322	Sequence 322, App
29	39.2	7	16	US-10-714-564A-305	Sequence 305, App
29	39.2	7	16	US-10-714-564A-323	Sequence 323, App
29	39.2	8	16	US-10-714-564A-306	Sequence 306, App
29	39.2	8	16	US-10-714-564A-324	Sequence 324, App
29	39.2	9	16	US-10-714-564A-307	Sequence 307, App
29	39.2	9	16	US-10-714-564A-325	Sequence 325, App
29	39.2	10	10	US-09-572-270A-162	Sequence 162, App
29	39.2	10	14	US-10-221-993-1	Sequence 1, Appli
29	39.2	10	16	US-10-714-564A-308	Sequence 308, App
29	39.2	10	16	US-10-714-564A-326	Sequence 326, App
31	39.2	11	9	US-09-912-609-24	Sequence 24, Appl
29	39.2	11	16	US-10-714-564A-309	Sequence 309, App
29	39.2	11	16	US-10-714-564A-327	Sequence 327, App
29	39.2	11	17	US-10-838-289-80	Sequence 80, Appl
29	39.2	12	14	US-10-190-082-556	Sequence 556, App
29	39.2	12	16	US-10-714-564A-310	Sequence 310, App
29	39.2	12	16	US-10-714-564A-328	Sequence 328, App
28	37.8	9	16	US-10-777-053-378	Sequence 378, App
28	37.8	9	16	US-10-837-217-378	Sequence 378, App
28	37.8	11	9	US-09-912-609-27	Sequence 27, Appl
28	37.8	11	17	US-10-838-289-83	Sequence 83, Appl
28	37.8	12	17	US-10-838-289-320	Sequence 320, App
28	37.8	12	17	US-10-607-595-263	Sequence 263, App
27.5	37.2	9	13	US-10-046-922-62	Sequence 62, Appl
27.5	37.2	9	17	US-10-363-205-162	Sequence 162, App
27	36.5	7	16	US-10-727-335-79	Sequence 79, Appl
27	36.5	9	9	US-09-832-723-94	Sequence 94, Appl
27	36.5	9	10	US-09-938-864-49	Sequence 49, Appl
27	36.5	9	10	US-09-938-864-131	Sequence 131, App
27	36.5	9	10	US-09-938-864-167	Sequence 167, App
27	36.5	9	10	US-09-938-864-258	Sequence 258, App
27	36.5	9	10	US-09-938-864-278	Sequence 278, App
27	36.5	9	10	US-09-791-477-49	Sequence 49, Appl
27	36.5	9	10	US-09-791-477-131	Sequence 131, App
27	36.5	9	10	US-09-791-477-167	Sequence 167, App
27	36.5	9	10	US-09-791-477-258	Sequence 258, App
27	36.5	9	10	US-09-791-477-278	Sequence 278, App
27	36.5	9	10	US-09-785-019-49	Sequence 49, Appl
27	36.5	9	10	US-09-785-019-131	Sequence 131, App
27	36.5	9	10	US-09-785-019-167	Sequence 167, App
27	36.5	9	10	US-09-785-019-258	Sequence 258, App
27	36.5	9	10	US-09-785-019-278	Sequence 278, App
27	36.5	9	14	US-10-125-635A-49	Sequence 49, Appl
27	36.5	9	14	US-10-125-635A-131	Sequence 131, App
27	36.5	9	14	US-10-125-635A-167	Sequence 167, App
27	36.5	9	14	US-10-125-635A-258	Sequence 258, App
27	36.5	9	14	US-10-125-635A-278	Sequence 278, App
27	36.5	9	14	US-10-002-603-49	Sequence 49, Appl
27	36.5	9	14	US-10-002-603-131	Sequence 131, App
27	36.5	9	14	US-10-002-603-167	Sequence 167, App
27	36.5	9	14	US-10-002-603-258	Sequence 258, App
27	36.5	9	14	US-10-002-603-278	Sequence 278, App
27	36.5	9	14	US-10-303-331-94	Sequence 94, Appl
27	36.5	9	14	US-10-195-835-49	Sequence 49, Appl
27	36.5	9	14	US-10-195-835-131	Sequence 131, App
27	36.5	9	14	US-10-195-835-167	Sequence 167, App
27	36.5	9	14	US-10-195-835-258	Sequence 258, App
27	36.5	9	14	US-10-195-835-278	Sequence 278, App
27	36.5	9	15	US-10-286-333-49	Sequence 49, Appl
27	36.5	9	15	US-10-286-333-131	Sequence 131, App
27	36.5	9	15	US-10-286-333-167	Sequence 167, App
27	36.5	9	15	US-10-286-333-258	Sequence 258, App
27	36.5	9	15	US-10-286-333-278	Sequence 278, App
27	36.5	9	15	US-10-244-830-49	Sequence 49, Appl

85 27 36.5 9 15 US-10-244-830-131 Sequence 131, App  
86 27 36.5 9 15 US-10-244-830-167 Sequence 167, App  
87 27 36.5 9 15 US-10-244-830-258 Sequence 258, App  
88 27 36.5 9 15 US-10-244-830-278 Sequence 278, App  
89 27 36.5 9 15 US-10-427-717-49 Sequence 49, Appl  
90 27 36.5 9 15 US-10-427-717-131 Sequence 131, App  
91 27 36.5 9 15 US-10-427-717-167 Sequence 167, App  
92 27 36.5 9 15 US-10-427-717-258 Sequence 258, App  
93 27 36.5 9 15 US-10-427-717-278 Sequence 278, App  
94 27 36.5 9 15 US-10-471-835-2 Sequence 2, Appl  
95 27 36.5 9 16 US-10-648-780-49 Sequence 49, Appl  
96 27 36.5 9 16 US-10-648-780-131 Sequence 131, App  
97 27 36.5 9 16 US-10-648-780-167 Sequence 167, App  
98 27 36.5 9 16 US-10-648-780-258 Sequence 258, App  
99 27 36.5 9 16 US-10-648-780-278 Sequence 278, App  
100 27 36.5 9 16 US-10-490-873-3 Sequence 3, Appl

## ALIGNMENTS

RESULT 1  
US-09-782-650-5  
; Sequence 5, Application US/09782650  
; Patent No. US20020019350A1  
; GENERAL INFORMATION:  
; APPLICANT: Levine, Arnold J.  
; APPLICANT: Mitterer, Artur  
; APPLICANT: Falkner, Falko-Guenter  
; APPLICANT: Scheiflinger, Friedrich  
; APPLICANT: Dörner, Friedrich  
; APPLICANT: Edwards Lifesciences Corporation  
; TITLE OF INVENTION: Targeted Angiogenesis  
; FILE REFERENCE: 20553D-000611US  
; CURRENT APPLICATION NUMBER: US/09/782,650  
; CURRENT FILING DATE: 2001-02-12  
; PRIOR APPLICATION NUMBER: US 09/324,079  
; PRIOR FILING DATE: 1999-06-01  
; PRIOR APPLICATION NUMBER: US 09/327,045  
; PRIOR FILING DATE: 1999-06-07  
; PRIOR APPLICATION NUMBER: PCT/US00/14988  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 24  
; SOFTWARE: PatentIn ver. 2.1  
; SEQ ID NO 5  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence:targeting  
US-09-782-650-5  
Query Match 100.0%; Score 74; DB 9; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRSWNKADNRSC 12  
Db 1 CRSWNKADNRSC 12  
RESULT 2  
US-09-910-582b-10  
; Sequence 10, Application US/09910582B  
; Publication No. US20030045476A1  
; GENERAL INFORMATION:  
; APPLICANT: Ruoslahti, Erkki  
; APPLICANT: Mackenna, Deirdre A.  
; TITLE OF INVENTION: Heart Homing Conjugates  
; FILE REFERENCE: P-LJ 4857  
; CURRENT APPLICATION NUMBER: US/09/910,582B  
; CURRENT FILING DATE: 2001-07-20

; PRIOR APPLICATION NUMBER: US 09/326,718  
; PRIOR FILING DATE: 1999-06-07  
; NUMBER OF SEQ ID NOS: 15  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 10  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: synthetic construct  
US-09-910-582B-10  
Query Match 100.0%; Score 74; DB 10; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRSWNKADNRSC 12  
Db 1 CRSWNKADNRSC 12  
RESULT 3  
US-10-838-289-38  
; Sequence 38, Application US/10838289  
; Publication No. US20050058603A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Jimming  
; APPLICANT: Ai, Hua  
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
; FILE REFERENCE: CRRU-P01-040  
; CURRENT APPLICATION NUMBER: US/10/838,289  
; CURRENT FILING DATE: 2004-05-03  
; PRIOR APPLICATION NUMBER: US 60/502,429  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: US 60/467,389  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 756  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 38  
; LENGTH: 12  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: Heart homing peptide  
US-10-838-289-38  
Query Match 100.0%; Score 74; DB 17; Length 12;  
Best Local Similarity 100.0%; Pred. No. 0.00011;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 CRSWNKADNRSC 12  
Db 1 CRSWNKADNRSC 12  
RESULT 4  
US-09-912-609-22  
; Sequence 22, Application US/09912609  
; Publication No. US20020041898A1  
; GENERAL INFORMATION:  
; APPLICANT: UNGER, EVAN C.  
; APPLICANT: MATSUNAGA, TERRY ONICHI  
; APPLICANT: RAMASWAMI, VARADARAJAN  
; APPLICANT: ROMANOWSKI, MAREK J.  
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS  
; FILE REFERENCE: 5030-0001-24  
; CURRENT APPLICATION NUMBER: US/09/912,609  
; CURRENT FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 09/703,474  
; PRIOR FILING DATE: 2000-10-31  
; PRIOR APPLICATION NUMBER: 09/478,124  
; PRIOR FILING DATE: 2000-01-05



; NUMBER OF SEQ ID NOS: 131  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 22  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-912-609-22

Query Match 45.9%; Score 34; DB 9; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12  
|:|:|:|:|  
Db 2 SFGKGNRIC 11

RESULT 5  
US-10-838-289-78  
; Sequence 78, Application US/10838289  
; Publication No. US20050058603A1  
; GENERAL INFORMATION:  
; APPLICANT: Ai, Hua  
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
; FILE REFERENCE: CWRU-P01-040  
; CURRENT APPLICATION NUMBER: US/10/838,289  
; CURRENT FILING DATE: 2004-05-03  
; PRIOR APPLICATION NUMBER: US 60/502,429  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: US 60/467,389  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 756  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 78  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: RGD-binding determinant homing peptide  
US-10-838-289-78

Query Match 45.9%; Score 34; DB 17; Length 11;  
Best Local Similarity 60.0%; Pred. No. 1.5e+02;  
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12  
|:|:|:|:|  
Db 2 SFGKGNRIC 11

RESULT 6  
US-09-912-609-25  
; Sequence 25, Application US/09912609  
; Publication No. US20020041898A1  
; GENERAL INFORMATION:  
; APPLICANT: UNGER, EVAN C.  
; APPLICANT: MATSUNAGA, TERRY ONICHI  
; APPLICANT: RAMASWAMI, VARADARAJAN  
; APPLICANT: ROMANOWSKI, MAREK J.  
; TITLE OF INVENTION: NOVEL TARGETED DELIVERY SYSTEMS FOR BIOACTIVE AGENTS  
; FILE REFERENCE: 5030-0001.24  
; CURRENT APPLICATION NUMBER: US/09/912,609  
; CURRENT FILING DATE: 2001-07-25  
; PRIOR APPLICATION NUMBER: 09/703,474  
; PRIOR FILING DATE: 2000-10-31  
; PRIOR APPLICATION NUMBER: 09/478,124  
; PRIOR FILING DATE: 2000-01-05  
; NUMBER OF SEQ ID NOS: 131

; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 25  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic  
; OTHER INFORMATION: peptide  
US-09-912-609-25

Query Match 43.2%; Score 32; DB 9; Length 11;  
Best Local Similarity 50.0%; Pred. No. 3e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12  
|:|:|:|:|  
Db 2 SFGGRDRNC 11

RESULT 7  
US-10-838-289-81  
; Sequence 81, Application US/10838289  
; Publication No. US20050058603A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Jinming  
; APPLICANT: Ai, Hua  
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
; FILE REFERENCE: CWRU-P01-040  
; CURRENT APPLICATION NUMBER: US/10/838,289  
; CURRENT FILING DATE: 2004-05-03  
; PRIOR APPLICATION NUMBER: US 60/502,429  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: US 60/467,389  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 756  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 81  
; LENGTH: 11  
; TYPE: PRT  
; ORGANISM: Unknown  
; FEATURE:  
; OTHER INFORMATION: RGD-binding determinant homing peptide  
US-10-838-289-81

Query Match 43.2%; Score 32; DB 17; Length 11;  
Best Local Similarity 50.0%; Pred. No. 3e+02;  
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 SWNKADNRSC 12  
|:|:|:|:|  
Db 2 SFGGRDRNC 11

RESULT 8  
US-10-838-289-301  
; Sequence 301, Application US/10838289  
; Publication No. US20050058603A1  
; GENERAL INFORMATION:  
; APPLICANT: Gao, Jinming  
; APPLICANT: Ai, Hua  
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER  
; FILE REFERENCE: CWRU-P01-040  
; CURRENT APPLICATION NUMBER: US/10/838,289  
; CURRENT FILING DATE: 2004-05-03  
; PRIOR APPLICATION NUMBER: US 60/502,429  
; PRIOR FILING DATE: 2003-09-12  
; PRIOR APPLICATION NUMBER: US 60/467,389  
; PRIOR FILING DATE: 2003-05-02  
; NUMBER OF SEQ ID NOS: 756  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 301

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; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Retina homing peptide
US-10-838-289-301

Query Match          43.2%; Score 32; DB 17; Length 12;
Best Local Similarity 41.7%; Pred. NO. 3.2e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 CRSWNKADNRSC 12
      | : | : |
Db      1 CORVNSVENASC 12

RESULT 9
US-10-607-595-244
; Sequence 244, Application US/10607595
; Publication No. US20050074812A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/10/607,595
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 244
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-244

Query Match          43.2%; Score 32; DB 17; Length 12;
Best Local Similarity 41.7%; Pred. NO. 3.2e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY      1 CRSWNKADNRSC 12
      | : | : |
Db      1 CORVNSVENASC 12

RESULT 10
US-10-492-929-13
; Sequence 13, Application US/10492929
; Publication No. US20050124544A1
; GENERAL INFORMATION:
; APPLICANT: GRANIER, CLAUDE
; APPLICANT: VILLARD, SYLVIE
; TITLE OF INVENTION: PEPTIDE DECOYS FOR THE PREPARATION OF MEDICAMENTS
; TITLE OF INVENTION: INTENDED FOR THE PREVENTION OR TREATMENT OF AUTOIMMUNE
; TITLE OF INVENTION: PATHOLOGIES, OR DISORDERS LINKED TO THE APPEARANCE OF
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST EXOGENOUS PROTEINS
; FILE REFERENCE: 0508-1103
; CURRENT APPLICATION NUMBER: US/10/492,929
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: PCT/FR02/03557
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: FR 01/13360
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 13
; LENGTH: 12
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; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-492-929-13

Query Match          43.2%; Score 32; DB 18; Length 12;
Best Local Similarity 33.3%; Pred. NO. 3.2e+02;
Matches 4; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY      1 CRSWNKADNRSC 12
      | : | : |
Db      1 CSKWHNRSKRHC 12

RESULT 11
US-10-838-289-189
; Sequence 189, Application US/10838289
; Publication No. US20050058603A1
; GENERAL INFORMATION:
; APPLICANT: Gao, Jimming
; APPLICANT: Ai, Hua
; TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
; TITLE OF INVENTION: NANOSHELLS
; FILE REFERENCE: CWRU-P01-040
; CURRENT APPLICATION NUMBER: US/10/838,289
; CURRENT FILING DATE: 2004-05-03
; PRIOR APPLICATION NUMBER: US 60/502,429
; PRIOR FILING DATE: 2003-09-12
; PRIOR APPLICATION NUMBER: US 60/467,389
; PRIOR FILING DATE: 2003-05-02
; NUMBER OF SEQ ID NOS: 756
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 189
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Lung homing peptide
US-10-838-289-189

Query Match          41.9%; Score 31; DB 17; Length 12;
Best Local Similarity 33.3%; Pred. NO. 4.6e+02;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY      1 CRSWNKADNRSC 12
      | : | : |
Db      1 CRPHNQAHTEC 12

RESULT 12
US-10-607-595-82
; Sequence 82, Application US/10607595
; Publication No. US20050074812A1
; GENERAL INFORMATION:
; APPLICANT: Ruoslahti, Erkki
; APPLICANT: Pasqualini, Renata
; TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
; TITLE OF INVENTION: Tissues
; FILE REFERENCE: P-LJ 4514
; CURRENT APPLICATION NUMBER: US/10/607,595
; CURRENT FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: US/09/722,250
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: US 09/042,107
; PRIOR FILING DATE: 1998-03-13
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 82
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
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; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-82

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Query Match	41.9%	Score 31;	DB 17;	Length 12;
Best Local Similarity	33.3%	Pred. No. 4.6e+02;		
Matches 4;	Conservative	2;	Mismatches 6;	Indels 0;
Gaps	0;			

Qy	1	CRSWNKADNRSC	12
		:	
Db	1	CRPWHNOAHTEC	12

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RESULT 13
US-10-492-929-16
; Sequence 16, Application US/10492929
; Publication No. US20050124544A1
; GENERAL INFORMATION:
; APPLICANT: GRANIER, CLAUDE
; APPLICANT: VILLARD, SYLVIE
; TITLE OF INVENTION: PEPTIDE DECOYS FOR THE PREPARATION OF MEDICAMENTS
; TITLE OF INVENTION: INTENDED FOR THE PREVENTION OR TREATMENT OF AUTOIMMUNE
; TITLE OF INVENTION: PATHOLOGIES, OR DISORDERS LINKED TO THE APPEARANCE OF
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST EXOGENOUS PROTEINS
; FILE REFERENCE: 0508-1103
; CURRENT APPLICATION NUMBER: US/10/492,929
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: PCT/FR02/03557
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: FR 01/13360
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-492-929-16

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Query Match	41.9%	Score 31;	DB 18;	Length 12;
Best Local Similarity	33.3%	Pred. No. 4.6e+02;		
Matches	4;	Conservative	2;	Mismatches 6;
				Indels 0;
				Gaps 0;

QY 1 CRSWNKADNRSC 12  
| | | : | |  
pb 1 CMKWSNRSSRWC 12

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RESULT 14
US-09-572-404B-2219
; Sequence 2219, Application US/09572404B
; Publication No. US20030078374A1
; GENERAL INFORMATION:
; APPLICANT: Proteom Ltd
; TITLE OF INVENTION: Complementary peptide ligands from the human genome
; FILE REFERENCE: Human patent
; CURRENT APPLICATION NUMBER: US/09/572,404B
; CURRENT FILING DATE: 2000-05-17
; NUMBER OF SEQ ID NOS: 4203
; SOFTWARE: ProtPatent version 1.0
; SEQ ID NO 2219
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: sequence located in C7 at 702-711 and may interact
; OTHER INFORMATION: this patent.
US-09-572-404B-2219

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Query Match

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Best Local Similarity 44.4%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
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Qy 1 CRSWNKADN 9  
| : | | |  
Db 1 CORWEKLQN 9

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RESULT 15
US-10-492-929--9
; Sequence 9, Application US/10492929
; Publication No. US20050124544A1
; GENERAL INFORMATION:
; APPLICANT: GRANIER, CLAUDE
; APPLICANT: VILLARD, SYLVIE
; TITLE OF INVENTION: PEPTIDE DECOYS FOR THE PREPARATION OF MEDICAMENTS
; TITLE OF INVENTION: INTENDED FOR THE PREVENTION OR TREATMENT OF AUTOIMMUNE
; TITLE OF INVENTION: PATHOLOGIES, OR DISORDERS LINKED TO THE APPEARANCE OF
; TITLE OF INVENTION: PATHOLOGIES, OR DISORDERS LINKED TO THE APPEARANCE OF
; TITLE OF INVENTION: ANTIBODIES DIRECTED AGAINST EXOGENOUS PROTEINS
; FILE REFERENCE: 0508-1103
; CURRENT APPLICATION NUMBER: US/10/492,929
; CURRENT FILING DATE: 2004-04-19
; PRIOR APPLICATION NUMBER: PCT/FR02/03557
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: FR 01/13360
; PRIOR FILING DATE: 2001-10-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-492-929--9

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Query Match	40.5%;	Score 30;	DB 18;	Length 12;
Best Local Similarity	41.7%;	Pred. No. 6.5e+02;		
Matches	5: Conservative	3: Mismatches	2: Indels	2: Gaps

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QY      1 CRSWNKADNRSC 12
        | : | : : |
Db      2 CHTW--SNRRSC 11
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Search completed: August 3, 2005, 12:53:14  
Job time : 153 secs

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